

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 2, 2000, 17:32:35 ; Search time 107.24 Seconds

Sequence: (without alignments) 1.876 Million cell updates/sec

Title: US-09-142-613-2

Perfect score: 62

Sequence: 1 KSGYSXPSPGT 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext. 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/prodata/1/aa/5A.COMB.pep:*

2: /cgn2_6/prodata/1/aa/5B.COMB.pep:*

3: /cgn2_6/prodata/1/aa/6.COMB.pep:*

4: /cgn2_6/prodata/1/aa/PCDRS.COMB.pep:*

5: /cgn2_6/prodata/1/aa/backfilest1.pep:*

Pred. No. 15 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	%	Match Length	DB ID	Description
1	58	93.5	31.2	US-09-244-951A-4	Sequence 4, Appl1	SEQUENCE 1
2	58	93.5	34.2	US-08-602-264A-10	Sequence 10, Appl1	SEQUENCE 2
3	58	93.5	34.3	US-08-641-018A-10	Sequence 10, Appl1	SEQUENCE 3
4	58	93.5	67.2	US-08-244-951A-1	Sequence 1, Appl1	SEQUENCE 4
5	58	93.5	67.2	US-08-244-951A-1	Sequence 1, Appl1	SEQUENCE 5
6	58	93.5	67.3	US-08-403-917A-1	Sequence 1, Appl1	SEQUENCE 6
7	58	93.5	106.3	US-08-776-360B-1	Sequence 1, Appl1	SEQUENCE 7
8	58	93.5	112.3	US-08-666-360-1	Sequence 2, Appl1	SEQUENCE 8
9	58	93.5	351.1	US-08-159-969-2	Sequence 2, Appl1	SEQUENCE 9
10	58	93.5	352.2	US-08-726-06A-17	Sequence 17, Appl1	SEQUENCE 10
11	58	93.5	391.2	US-08-244-951A-10	Sequence 10, Appl1	SEQUENCE 11
12	58	93.5	391.2	US-08-389-011-23	Sequence 23, Appl1	SEQUENCE 12
13	58	93.5	391.3	US-08-403-917A-23	Sequence 23, Appl1	SEQUENCE 13
14	56	90.9	27.2	US-08-244-951A-5	Sequence 3, Appl1	SEQUENCE 14
15	39	62.9	252.1	US-08-411-777-8	Sequence 8, Appl1	SEQUENCE 15
16	39	62.9	252.3	US-09-057-088-8	Sequence 8, Appl1	SEQUENCE 16
17	39	62.9	427.1	US-08-956-700B-3	Sequence 10, Appl1	SEQUENCE 17
18	39	62.9	427.1	US-08-476-537-3	Sequence 23, Appl1	SEQUENCE 18
19	39	62.9	427.1	US-08-485-507-3	Sequence 23, Appl1	SEQUENCE 19
20	39	62.9	427.2	US-08-475-879-3	Sequence 3, Appl1	SEQUENCE 20
21	39	62.9	427.4	US-08-611-107-6	Sequence 3, Appl1	SEQUENCE 21
22	39	62.9	447.2	US-08-422-560A-6	Sequence 8, Appl1	SEQUENCE 22
23	37	59.7	455.1	US-08-035-28-2	Sequence 35, Appl1	SEQUENCE 23
24	37	59.7	545.2	US-08-990-114-1	Sequence 2, Appl1	SEQUENCE 24
25	37	58.9	788.1	US-08-194-338-12	Sequence 12, Appl1	SEQUENCE 25
26	36.5	58.9	836.1	US-08-836-561-106	Sequence 106, Appl1	SEQUENCE 26
27	36	58.1	313.3	US-08-836-561-106	Sequence 2, Appl1	SEQUENCE 27
28	1	58.1	335.1	US-07-947-130-2	Sequence 1, Appl1	SEQUENCE 28

ALIGNMENTS

29	35	59.1	335.1	US-08-421-822-2	Sequence 2, Appl1
30	36	58.1	335.1	US-08-421-823-2	Sequence 2, Appl1
31	36	58.1	359.1	US-08-120-827-2	Sequence 2, Appl1
32	36	58.1	359.1	US-08-478-675-2	Sequence 2, Appl1
33	36	58.1	396.1	US-07-757-390-14	Sequence 14, Appl1
34	36	58.1	396.1	US-08-422-282-14	Sequence 14, Appl1
35	36	58.1	396.1	US-08-442-281-14	Sequence 14, Appl1
36	36	58.1	396.2	US-08-939-727-13	Sequence 13, Appl1
37	36	58.1	396.2	US-01-476-537-6	Sequence 6, Appl1
38	36	58.1	420.1	US-07-757-390-13	Sequence 13, Appl1
39	36	58.1	420.1	US-08-442-282-13	Sequence 13, Appl1
40	36	58.1	420.2	US-08-939-727-13	Sequence 13, Appl1
41	36	58.1	420.2	US-01-476-537-6	Sequence 6, Appl1
42	36	58.1	453.1	US-01-476-537-6	Sequence 6, Appl1
43	36	58.1	453.1	US-08-485-607-5	Sequence 6, Appl1
44	36	58.1	453.1	US-08-611-107-8	Sequence 8, Appl1
45	36	58.1	453.1	US-08-611-107-8	Sequence 8, Appl1

Query Match 93.5%; Score 58; DB 2; Length 31;
 Best Local Similarity 83.3%; Pred. No. 0.0035; 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Mismatches 0; Qy 1 KSGYSXPSPGT 12
 Db 4 RSGYSSPGSPGT 15

RESULT 2
 US-08-602-264A-10
 Sequence 10; Application US/08602264A
 Patent No. 5837553

GENERAL INFORMATION:
 APPLICANT: AKIHICO TAKASHIMA et al.
 TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
 TITLE OF INVENTION: ALZHEIMER'S DISEASE, A SCREENING METHOD OF ALZHEIMER'S DISEASE
 NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
 ADDRESSEE: WENDEROTH, LIND & PONACK
 STREET: 805 Fifteenth Street, N.W., #700
 CITY: Washington
 COUNTRY: D.C.
 ZIP: 20005

COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/461,018A
 FILING DATE: June 5, 1995
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/204,091
 FILING DATE: February 20, 1996

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/602-264A
 FILING DATE: March 2, 1994

ATTORNEY/AGENT INFORMATION:
 NAME: Warren M. Cheek, Jr.
 REGISTRATION NUMBER: 33,367
 REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
 TELEPHONE:
 TELEX:
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34 amino acids

TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

US-08-61018A-10

Query Match 93.5%; Score 58; DB 3; Length 34;
 Best Local Similarity 83.3%; Pred. No. 0.0039; 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Mismatches 0; Qy 1 KSGYSXPSPGT 12
 Db 4 RSGYSSPGSPGT 15

RESULT 4
 US-08-244-951A-1
 Sequence 1; Application US/08244951A
 Patent No. 5843779

GENERAL INFORMATION:
 APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
 TITLE OF INVENTION: MONOClonal ANTIBODIES
 TITLE OF INVENTION: DIRECTED AGAINST THE MICROBULE ASSOCIATED
 TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
 TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
 NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRLMAN & MUSERLIM
 STREET: 600 THIRD AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016

COMPUTER READABLE FORM:
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/244,951A
 FILING DATE: 19-JAN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP93/03499
 FILING DATE: 10-DEC-1993
 PRIORITY APPLICATION DATA:
 REFERENCE/DOCKET NUMBER: EP/92/403403.6
 ATTORNEY/AGENT INFORMATION:
 NAME: CHARLES A. MUSERLIAN
 REGISTRATION NUMBER: 19,683
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 661-8000
 TELEFAX: (212) 661-8002
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 67
 TYPE: Amino Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown

FEATURE:
 NAME/KEY: human tau protein 155-211
 US-08-244,951A-1

RESULT 5
 Query Match 93.5%; Score 58; DB 2; Length 67;
 Best Local Similarity 83.3%; Pred. No. 0.0079; 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGSYXPGSPGT 12
 Db 40 RSGYSSGSPGT 51

RESULT 6
 Query Match 93.5%; Score 58; DB 2; Length 67;
 Best Local Similarity 83.3%; Pred. No. 0.0079; 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGSYXPGSPGT 12
 Db 40 RSGYSSGSPGT 51

RESULT 6
 Query Match 93.5%; Score 58; DB 2; Length 67;
 Best Local Similarity 83.3%; Pred. No. 0.0079; 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KGSYXPGSPGT 12
 Db 40 RSGYSSGSPGT 51

GENERAL INFORMATION:
 APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
 APPLICANT: VANMECHELEN, EUGENE;
 APPLICANT: VAN DE VOORDE, ANDRE
 TITLE OF INVENTION: MONOClonAL ANTIBODIES
 TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
 TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
 TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
 TITLE OF INVENTION: MONOClonAL ANTIBODIES AND THEIR APPLICATIONS.
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRMAN & MUSERLIAN
 STREET: 600 THIRD AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/403,917A
 FILING DATE: 19-JAN-1995
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/256,167
 FILING DATE: 27-JUN-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/244,951
 FILING DATE: 13-JUN-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP93/03499
 FILING DATE: 10-DEC-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: EP/92/403403.6
 FILING DATE: 14-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.003-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 67

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

US-08-403-917A-1

RESULT 7

US-08-776-404B-1

Sequence 1, Application US/08776404B

Patent No. 612103

GENERAL INFORMATION:

APPLICANT: VANMECHELLEN, EUGENE

TITLE OF INVENTION: MONOClonal antibodies specific for an epitope of

TITLE OF INVENTION: A PARTICULAR SUBCLASS OR FORM OF PHOSPHORYLATED TAU,

TITLE OF INVENTION: HYBRIDOMAS SECRETING THEM, ANTIGEN RECOGNITION OF THESE

TITLE OF INVENTION: ANTIBODIES AND THEIR APPLICATIONS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE & DURKEE

STREET: P.O. BOX 4433

CITY: HOUSTON

STATE: TEXAS

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Microsoft Word 6.0 / ASCII text output

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,404B

FILING DATE: 27 Jan 1997

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/03032

FILING DATE: 31 Jul 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94870131.3

FILING DATE: 29 Jul 1994

ATTORNEY/AGENT INFORMATION:

NAME: KAMMERER, PATRICIA A.

REGISTRATION NUMBER: 29,775

REFERENCE/DOCKET NUMBER: INNS:003

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: linear

MOLECULE TYPE: peptide

US-08-776-404B-1

RESULT 8

US-08-666-360-1

Sequence 1, Application US/08666360

Patent No. 6008124

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Monoclonal antibodies specific for PHF-tau, antigen recognition of these

TIME OF INVENTION: hybridomas secreting them, antigen recognition of these

TITLE OF INVENTION: antibodies and their applications

NUMBER OF SEQUENCES: 3

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/666,360

FILING DATE:

CLASSIFICATION: 435

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: peptide

US-08-666-360-1

RESULT 9

US-08-159-969-2

Sequence 2, Application US/08159969

Patent No. 5492812

GENERAL INFORMATION:

APPLICANT: Vornheis, Paul H.

TITLE OF INVENTION: Diagnostic Method for Alzheimer's

TITLE OF INVENTION: Disease

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/159,969

FILING DATE:

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/138,778

FILING DATE:

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/138,778

FILING DATE:

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/138,778

FILING DATE:

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/138,778

FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 46997-040
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9050
 TELEFAX: 212 869-8864/9741
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 351 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

RESULT 10
 US-08-726-306A-17
 ; Sequence 17, Application US/08726306A
 ;
 GENERAL INFORMATION:
 APPLICANT: van Leeuwen, Frederik Willem
 APPLICANT: Burbach, Johannes Peter Henri
 APPLICANT: Grosvald, Franklin G.
 TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
 NUMBER OF SEQUENCES: 189
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Banner & Witcoff, Ltd.
 STREET: 1 Financial Center
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect 6.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/726,306A
 FILING DATE: 02-Oct-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 95/20080,4
 FILING DATE: 02-Oct-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/009,832
 FILING DATE: 01-Jan-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams, Ph.D., Kathleen M.
 REGISTRATION NUMBER: 34,380
 REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 345-9100
 TELEFAX: (617) 345-9111
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 352 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: protein

RESULT 11
 US-08-244-951A-10
 Sequence 10, Application US/08244951A
 ;
 Patent No. 5843779
 GENERAL INFORMATION:
 APPLICANT: VANDRMEEREN, MARC; MERCKEN, MARC;
 APPLICANT: VANMERHELEN, EUGENE; VAN DE VOERDE, ANDRE
 TITLE OF INVENTION: MONOClonAL ANTIBODIES
 TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
 TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
 TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
 TITLE OF INVENTION: MONOClonAL ANTIBODIES AND THEIR APPLICATIONS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIERNAN & MUSERLIAN
 STREET: 600 THIRD AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/244,951A
 FILING DATE: 19-JAN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP93/03499
 FILING DATE: 10-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP/92/403403.6
 FILING DATE: 14-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: CHARLES A. MUSERLIAN
 REGISTRATION NUMBER: 19,683
 REFERENCE/DOCKET NUMBER: 410.003A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 661-8000
 TELEFAX: (212) 661-002
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 391
 TYPE: Amino Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown
 FEATURE:
 NAME/KEY: mTHFMPH-tau fusion protein
 US-08-244-951A-10

Query Match 93.5%; Score 58; DB 2; Length 352;
 Best Local Similarity 83.3%; Pred. No. 0.045; 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSGYSXPSPGT 12
 Db 136 RSGYSSPGSPGT 147

RESULT 12
 US-08-244-951A-10
 Sequence 10, Application US/08244951A
 ;
 Patent No. 5843779
 GENERAL INFORMATION:
 APPLICANT: VANDRMEEREN, MARC; MERCKEN, MARC;
 APPLICANT: VANMERHELEN, EUGENE; VAN DE VOERDE, ANDRE
 TITLE OF INVENTION: MONOClonAL ANTIBODIES
 TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
 TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
 TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
 TITLE OF INVENTION: MONOClonAL ANTIBODIES AND THEIR APPLICATIONS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIERNAN & MUSERLIAN
 STREET: 600 THIRD AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/244,951A
 FILING DATE: 19-JAN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP93/03499
 FILING DATE: 10-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP/92/403403.6
 FILING DATE: 14-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: CHARLES A. MUSERLIAN
 REGISTRATION NUMBER: 19,683
 REFERENCE/DOCKET NUMBER: 410.003A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 661-8000
 TELEFAX: (212) 661-002
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 391
 TYPE: Amino Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown
 FEATURE:
 NAME/KEY: mTHFMPH-tau fusion protein
 US-08-244-951A-10

Query Match 93.5%; Score 58; DB 2; Length 391;
 Best Local Similarity 83.3%; Pred. No. 0.051; 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSGYSXPSPGT 12
 Db 175 RSGYSSPGSPGT 186

RESULT 12

US-08-389-011-23

Sequence 23, Application US/08389011

Patent No. 5861257

GENERAL INFORMATION:

APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;

TITLE OF INVENTION: MONOCLONAL ANTIBODIES

TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED

TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION

TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS: BIERMAN & MUSERLIAN

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10016

COMPUTER READABLE FORM:

COMPUTER: IBM PC COMPATIBLE

MEDIUM TYPE: FLOPPY DISK

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/389,011

FILING DATE: 15-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,916

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

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FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,917A

FILING DATE: 19-JAN-1995

SEQUENCE CHARACTERISTICS:

LENGTH: 391

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

SEQUENCE CHARACTERISTICS:

LENGTH: 391

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

Query Match 93.5%; Score 58; DB 2; Length 391; Best Local Similarity 83.3%; Pred. No. 0.051; 1; Indels 0; Gaps 0;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 14

US-08-244-951A-5

Sequence 5, Application US/08244951A

Patent No. 5843779

GENERAL INFORMATION:

APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;

TITLE OF INVENTION: MONOCLONAL ANTIBODIES

TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED

TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE

TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS

RESULT 13

US-08-403-917A-23

Sequence 23, Application US/08403917A

Patent No. 6010913

GENERAL INFORMATION:

NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIERMAN & MUSERLIAN
 STREET: 600 THIRD AVENUE
 CITY: NEW YORK
 STATE: NY
 COUNTRY: USA
 ZIP: 10016
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/244,951A
 FILING DATE: 19-JAN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP93/03499
 FILING DATE: 10-DEC-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: EP/92/403403.6
 FILING DATE: 14-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: CHARLES A. MUSERLIAN
 REGISTRATION NUMBER: 19,683
 REFERENCE/DOCKET NUMBER: 410.003A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 661-8000
 TELEFAX: (212) 661-8002
 INFORMATION FOR SEQ ID NO: 5:
 LENGTH: 27
 SEQUENCE CHARACTERISTICS:
 TYPE: Amino Acid
 STRANDEDNESS: Unknown
 TOPOGONY: Linear
 MOLECULE TYPE: No. 5792641e
 US-08-244-951A-5

RESULT 15
 US-08-411-77-8
 Sequence 8, Application US/08411777
 ; Patent No. 5792641
 GENERAL INFORMATION:
 APPLICANT: Schulein, Martin
 APPLICANT: Fredholm, Henrik
 APPLICANT: Hjorth, Carsten
 APPLICANT: Rasmussen, Grethe
 APPLICANT: Nielsen, Egon
 APPLICANT: Rosholm, Peter
 TITLE OF INVENTION: Cellulase Variants
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 5792641disk of No. 5792641th America
 STREET: 405 Lexington Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10174-6401
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/411,777
 FILING DATE: 05-MAY-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: Gregg, Valeta A.
 REGISTRATION NUMBER: 35,127
 REFERENCE/DOCKET NUMBER: 3913.504-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-867-0123
 TELEFAX: 212-868-9655
 TELEX:
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 252 amino acids
 STRANDEDNESS: single
 TYPE: amino acid
 TOPOGONY: linear
 MOLECULE TYPE: No. 5792641e
 US-08-411-77-8

Query	Match	Score	DB	Length
Qy	SGYSXGSPGT 12	62.9%	1	252;
Db	SGYSSPGSPGT 13	54.5%	2;	Mismatches
		2;	3;	Indels
			0;	Gaps
			0;	0;

Query	Match	Score	DB	Length
Qy	SGYSXGSPGT 12	39	1	252;
Db	SGYSSPGSPGT 13	39	1	252;
		0	0	0;

Search completed: October 2, 2000, 18:03:51
 Job time: 1876 sec

Tue Oct 3 09:21:58 2000

us-09-142-613-2.rai

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: October 2, 2000, 18:02:13 ; Search time 84.99 Seconds
(without alignments)

4.375 Million cell updates/sec

Title: perfect score: US-09-142-613-2

Sequence: 62 KSGYSXPGSPGT 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 85661 seqs, 30989116 residues

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : SwissProt 38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	58	TAU3_MOUSE	1	TAN3_MOUSE	P10637 mus musculu
2	58	TAU2_MOUSE	1	TAN2_MOUSE	P10638 mus musculu
3	58	TAU3_BOVIN	1	TAN3_BOVIN	P29173 bos tauris
4	58	TAU1_RAT	1	TAN1_RAT	P19332 rattus norv
5	58	TAU_HUMAN	1	TAN1_HUMAN	P10636 homo sapien
6	58	TAU_BOVIN	1	TAN1_BOVIN	P29172 bos tauris
7	67.7	TAU_EMENTI	1	TAN1_EMENTI	P03149 emericella
8	66.1	SYMP_PODAN	1	TAN1_PODAN	P28669 podospora a
9	66.1	YQ06_CAEEL	1	TAN1_CAEEL	Q09457 caenorhabdi
10	64.5	CALA_MOUSE	1	TAN1_MOUSE	Q05306 mus musculu
11	64.5	PING6_HUMAN	1	TAN1_HUMAN	P01178 homo sapien
12	64.5	RGC6_RAT	1	TAN1_RAT	P08774 rattus norv
13	64.5	Y505_CAEEL	1	TAN1_CAEEL	P17139 caenorhabdi
14	64.5	CA14_CAEEL	1	TAN1_CAEEL	P17140 caenorhabdi
15	62.9	ACCC_ANASP	1	TAN1_ANASP	Q06862 anaerena sp
16	62.9	GUBB_PSEFL	1	TAN1_PSEFL	P18126 pseudomonas
17	62.9	MRC2_KLEBN	1	TAN1_KLEBN	P21647 klebsiella
18	61.3	CAIA_HUMAN	1	TAN1_HUMAN	Q03692 homo sapien
19	61.3	Y505_CAEEL	1	TAN1_CAEEL	P01030 caenorhabdi
20	59.7	GAD_MOUSE	1	TAN1_MOUSE	P22933 mus musculu
21	59.7	GAD_RAT	1	TAN1_RAT	P18506 rattus norv
22	59.7	CA28_HUMAN	1	TAN1_HUMAN	P25067 homo sapien
23	59.7	CA28_ASCEU	1	TAN1_ASCEU	P27393 ascaris suu
24	59.7	MAP2_HUMAN	1	TAN1_HUMAN	P11137 homo sapien
25	59.7	MAP2_MOUSE	1	TAN1_MOUSE	P20357 mus musculu
26	59.7	MAP2_RAT	1	TAN1_RAT	P15146 rattus norv
27	58.1	RCLL_CHIAU	1	TAN1_CHIAU	P11695 chloroflexu
28	58.1	VEG_PAPAV	1	TAN1_PAPAV	P11329 europea el
29	58.1	NTRL_HUMAN	1	TAN1_HUMAN	P30989 homo sapien
30	58.1	ILUR_HUMAN	1	TAN1_HUMAN	Q01344 homo sapien
31	58.1	FIR4_RAT	1	TAN1_RAT	P06399 rattus norv
32	58.1	MGR_DRONE	1	TAN1_DRONE	P91685 drosophila
33	58.1	GLSI YEAST	1	TAN1_YEAST	P38631 saccharomy

ALIGNMENTS

RESULT	1	TAU3_MOUSE	STANDARD;	PRT;	341 AA.
RU	ID	TAU3_MOUSE			
CC	AC	P10637			
CC	DT	01-JUL-1989	(Rel. 11, Created)		
CC	DT	01-JUL-1989	(Rel. 11, Last sequence update)		
CC	DT	15-DEC-1998	(Rel. 37, Last annotation update)		
DE	DE		MICROTUBULE-ASSOCIATED PROTEIN TAU (CLONE TAU)		
GN	GN		MAPT OR MAPT.		
OS	OS		Mus musculus (Mouse)		
OC	OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; Mammalia		
RN	RN		[1]		
RP	RP		SEQUENCE FROM N.A.		
RX	RX		TISSUE-BRAIN;		
RA	RA		MEIDIM; 8809510.		
R1	R1		Lee G., Cowan N.J., Kirschner M.; "The Primary structure and heterogeneity of tau protein from mouse brain,"		
RT	RT		Science, 239:285-288 (1988).		
RU	RU		-I- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES		
CC	CC		MICROTUBULES.		
CC	CC		-I- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE		
CC	CC		PRODUCED BY ALTERNATIVE SPLICING.		
CC	CC		-I- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.		
CC	CC		-I- PPM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED		
CC	CC		BY CAMP KINASE.		
CC	CC		-I- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.		
CC	CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation in the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licensee@lsb-sib.ch).		
CC	CC		-----		
DR	DR		EMBL: M18775; AAA0165.1; -.		
DR	DR		PIR; B28820.		
DR	DR		MGD; MGIC:97180; MTAP.		
DR	DR		PFAM: PF00418; tubulin-binding; 3.		
DR	DR		PROTM: PS00229; TAU_MAP_1; 3.		
KW	KW		MICROTUBULES; Repeat; Alternative splicing.		
PT	PT		REPEAT; 175 205 TAU/MAP MOTIF.		
PT	PT		REPEAT; 206 235 TAU/MAP MOTIF.		
PT	PT		REPEAT; 237 268 TAU/MAP MOTIF.		
SQ	SQ		SEQUENCE 341 AA; 35714 MW; 478641931A5A143 CRC64;		
			Query Match 93.5%; Score 58; DB 1; Length 341;		
			Best Local Similarity 83.3%; Pred. No. 0.015; 1; Mismatches 1; Indels 0; Gaps 0;		
QY	QY		1 KSGYSXPGSPGT 12		
Db	Db		125 RGGYSSPGSPGT 136		

RL J. Cell Biol. 109:1173-1184(1989);
 CC 1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
 CC MICROTUBULES.
 CC -I- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
 CC PRODUCED BY ALTERNATIVE SPlicing.
 CC -I- DOMAIN: THE REPEATED DOMAIN Binds TO TUBULIN.
 CC -I- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
 CC BY CAMP KINASE.
 CC -I- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
 DR PIR; JS0306; JS0306.
 DR A33574; A33574.
 DR PFAM; PF00418; tubulin-binding; 4.
 DR PROSITE; PS00229; TAU_MAP1; 4.
 KW MICROTUBULES; Repeat; Alternative splicing; Phosphorylation.
 FT REPEAT 235 265 TAU/MAP MOTIF.
 FT REPEAT 266 296 TAU/MAP MOTIF.
 FT REPEAT 297 327 TAU/MAP MOTIF.
 FT REPEAT 328 359 TAU/MAP MOTIF.
 FT DISULFID 282 313 BY SIMILARITY.
 FT MOD_RES 347 347 PROSPHORYLATION (BY CAPK1) (POTENTIAL).
 FT VARSPICE 266 296 MISSING (IN FETAL ISOFORM).
 SQ SEQUENCE 432 AA: 45113 MW: A4810DF6CF04457F CRC64;

 Query Match 93.5%; Score 58; DB 1; Length 432;
 Best Local Similarity 83.3%; Pred. No. 0.019; 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Gaps 0;
 ID TAU_HUMAN STANDARD; PRD; 441 AA.
 AC P10536; P10518; Q14799; Q15551;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN TAU.
 GN MAPT OR MTB1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE; 93041757.
 RA Andreais A.; Brown W.M.; Kosik K.S.;
 RT "Structure and novel exons of the human tau gene."; Biochemistry 31:10626-10633(1992).
 RL [2] SEQUENCE FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 89351564.
 RA Goedert M.; Spillantini M.G.; Potier M.C.; Ulrich J.; Crowther R.A.;
 RT "Cloning and sequencing of the cDNA encoding an isoform of microtubule-associated protein tau containing four tandem repeats: differential expression of tau protein mRNAs in human brain."; EMBO J. 8:393-399(1989).
 RL [3] SEQUENCE OF 1-26 AND 306-441 FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 88034557.
 RA Goedert M.; Wischik C.; Crowther R.; Walker J.; Klug A.;
 RT "Cloning and sequencing of the cDNA encoding a core protein of the paired helical filament of Alzheimer disease: identification as the microtubule-associated protein tau"; Proc. Natl. Acad. Sci. U.S.A. 85:4051-4055(1988).
 RL [4] SEQUENCE OF 1-26 AND 306-441 FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 90180482.

 RESULT 5
 ID TAU_HUMAN STANDARD; PRD; 441 AA.
 AC P10536; P10518; Q14799; Q15551;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN TAU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE; 93041757.
 RA Andreais A.; Brown W.M.; Kosik K.S.;
 RT "Structure and novel exons of the human tau gene."; Biochemistry 31:10626-10633(1992).
 RL [2] SEQUENCE FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 89351564.
 RA Goedert M.; Spillantini M.G.; Potier M.C.; Ulrich J.; Crowther R.A.;
 RT "Cloning and sequencing of the cDNA encoding an isoform of microtubule-associated protein tau containing four tandem repeats: differential expression of tau protein mRNAs in human brain."; EMBO J. 8:393-399(1989).
 RL [3] SEQUENCE OF 1-26 AND 306-441 FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 88034557.
 RA Goedert M.; Wischik C.; Crowther R.; Walker J.; Klug A.;
 RT "Cloning and sequencing of the cDNA encoding a core protein of the paired helical filament of Alzheimer disease: identification as the microtubule-associated protein tau"; Proc. Natl. Acad. Sci. U.S.A. 85:4051-4055(1988).
 RL [4] SEQUENCE OF 1-26 AND 306-441 FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 90180482.

 Query Match 93.5%; Score 58; DB 1; length 441;
 Best Local Similarity 83.3%; Pred. No. 0.019; 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Gaps 0;
 ID TAU_HUMAN STANDARD; PRD; 441 AA.
 AC P10536; P10518; Q14799; Q15551;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN TAU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE; 93041757.
 RA Andreais A.; Brown W.M.; Kosik K.S.;
 RT "Structure and novel exons of the human tau gene."; Biochemistry 31:10626-10633(1992).
 RL [2] SEQUENCE FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 89351564.
 RA Goedert M.; Spillantini M.G.; Potier M.C.; Ulrich J.; Crowther R.A.;
 RT "Cloning and sequencing of the cDNA encoding an isoform of microtubule-associated protein tau containing four tandem repeats: differential expression of tau protein mRNAs in human brain."; EMBO J. 8:393-399(1989).
 RL [3] SEQUENCE OF 1-26 AND 306-441 FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 88034557.
 RA Goedert M.; Wischik C.; Crowther R.; Walker J.; Klug A.;
 RT "Cloning and sequencing of the cDNA encoding a core protein of the paired helical filament of Alzheimer disease: identification as the microtubule-associated protein tau"; Proc. Natl. Acad. Sci. U.S.A. 85:4051-4055(1988).
 RL [4] SEQUENCE OF 1-26 AND 306-441 FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 90180482.

 Lee G.; Neve R.L.; Kosik K.S.; "The microtubule binding domain of tau protein." ; Neuron 2:1161-1164(1989).
 RL J. Cell Biol. 109:1173-1184(1989);
 CC 1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
 CC MICROTUBULES.
 CC -I- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
 CC PRODUCED BY ALTERNATIVE SPlicing.
 CC -I- DOMAIN: THE REPEATED DOMAIN Binds TO TUBULIN.
 CC -I- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
 DR PIR; JS0306; JS0306.
 DR A33574; A33574.
 DR PFAM; PF00418; tubulin-binding; 4.
 DR PROSITE; PS00229; TAU_MAP1; 4.
 KW MICROTUBULES; Repeat; Alternative splicing; Phosphorylation.
 FT REPEAT 235 265 TAU/MAP MOTIF.
 FT REPEAT 266 296 TAU/MAP MOTIF.
 FT REPEAT 297 327 TAU/MAP MOTIF.
 FT REPEAT 328 359 TAU/MAP MOTIF.
 FT DISULFID 282 313 BY SIMILARITY.
 FT MOD_RES 347 347 PROSPHORYLATION (BY CAPK1) (POTENTIAL).
 FT VARSPICE 266 296 MISSING (IN FETAL ISOFORM).
 FT VARSPICE 275 305 MISSING (IN ISOFORM 1 AND ISOFORM 3).
 FT VARSPICE 275 305 MISSING (IN ISOFORM 2 AND ISOFORM 3).
 FT VARSPICE 1 44 MAERQEEFEMDHAFTGTYGIGDRKQDGHHQHODDEGDTDA GLR -> MRLQQRK (IN FETAL ISOFORM).
 FT VARSPICE 278 308 MISSING (IN FETAL ISOFORM).
 SQ SEQUENCE 441 AA: 45580 MW: 835A8706DB847A8CC CRC64;

 Query Match 93.5%; Score 58; DB 1; length 441;
 Best Local Similarity 83.3%; Pred. No. 0.019; 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Gaps 0;
 ID TAU_HUMAN STANDARD; PRD; 441 AA.
 AC P10536; P10518; Q14799; Q15551;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN TAU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE; 93041757.
 RA Andreais A.; Brown W.M.; Kosik K.S.;
 RT "Structure and novel exons of the human tau gene."; Biochemistry 31:10626-10633(1992).
 RL [2] SEQUENCE FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 89351564.
 RA Goedert M.; Spillantini M.G.; Potier M.C.; Ulrich J.; Crowther R.A.;
 RT "Cloning and sequencing of the cDNA encoding an isoform of microtubule-associated protein tau containing four tandem repeats: differential expression of tau protein mRNAs in human brain."; EMBO J. 8:393-399(1989).
 RL [3] SEQUENCE OF 1-26 AND 306-441 FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 88034557.
 RA Goedert M.; Wischik C.; Crowther R.; Walker J.; Klug A.;
 RT "Cloning and sequencing of the cDNA encoding a core protein of the paired helical filament of Alzheimer disease: identification as the microtubule-associated protein tau"; Proc. Natl. Acad. Sci. U.S.A. 85:4051-4055(1988).
 RL [4] SEQUENCE OF 1-26 AND 306-441 FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 90180482.

 Lee G.; Neve R.L.; Kosik K.S.; "The microtubule binding domain of tau protein." ; Neuron 2:1161-1164(1989).
 RL J. Cell Biol. 109:1173-1184(1989);
 CC 1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
 CC MICROTUBULES.
 CC -I- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
 CC PRODUCED BY ALTERNATIVE SPlicing.
 CC -I- DOMAIN: THE REPEATED DOMAIN Binds TO TUBULIN.
 CC -I- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
 DR PIR; JS0306; JS0306.
 DR A33574; A33574.
 DR PFAM; PF00418; tubulin-binding; 4.
 DR PROSITE; PS00229; TAU_MAP1; 4.
 KW MICROTUBULES; Repeat; Alternative splicing; Phosphorylation.
 FT REPEAT 235 265 TAU/MAP MOTIF.
 FT REPEAT 266 296 TAU/MAP MOTIF.
 FT REPEAT 297 327 TAU/MAP MOTIF.
 FT REPEAT 328 359 TAU/MAP MOTIF.
 FT DISULFID 282 313 BY SIMILARITY.
 FT MOD_RES 347 347 PROSPHORYLATION (BY CAPK1) (POTENTIAL).
 FT VARSPICE 266 296 MISSING (IN FETAL ISOFORM).
 FT VARSPICE 275 305 MISSING (IN ISOFORM 1 AND ISOFORM 3).
 FT VARSPICE 275 305 MISSING (IN ISOFORM 2 AND ISOFORM 3).
 FT VARSPICE 1 44 MAERQEEFEMDHAFTGTYGIGDRKQDGHHQHODDEGDTDA GLR -> MRLQQRK (IN FETAL ISOFORM).
 FT VARSPICE 278 308 MISSING (IN FETAL ISOFORM).
 SQ SEQUENCE 441 AA: 45580 MW: 835A8706DB847A8CC CRC64;

 Query Match 93.5%; Score 58; DB 1; length 441;
 Best Local Similarity 83.3%; Pred. No. 0.019; 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Gaps 0;
 ID TAU_HUMAN STANDARD; PRD; 441 AA.
 AC P10536; P10518; Q14799; Q15551;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN TAU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE; 93041757.
 RA Andreais A.; Brown W.M.; Kosik K.S.;
 RT "Structure and novel exons of the human tau gene."; Biochemistry 31:10626-10633(1992).
 RL [2] SEQUENCE FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 89351564.
 RA Goedert M.; Spillantini M.G.; Potier M.C.; Ulrich J.; Crowther R.A.;
 RT "Cloning and sequencing of the cDNA encoding an isoform of microtubule-associated protein tau containing four tandem repeats: differential expression of tau protein mRNAs in human brain."; EMBO J. 8:393-399(1989).
 RL [3] SEQUENCE OF 1-26 AND 306-441 FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 88034557.
 RA Goedert M.; Wischik C.; Crowther R.; Walker J.; Klug A.;
 RT "Cloning and sequencing of the cDNA encoding a core protein of the paired helical filament of Alzheimer disease: identification as the microtubule-associated protein tau"; Proc. Natl. Acad. Sci. U.S.A. 85:4051-4055(1988).
 RL [4] SEQUENCE OF 1-26 AND 306-441 FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 90180482.

 Lee G.; Neve R.L.; Kosik K.S.; "The microtubule binding domain of tau protein." ; Neuron 2:1161-1164(1989).
 RL J. Cell Biol. 109:1173-1184(1989);
 CC 1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
 CC MICROTUBULES.
 CC -I- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
 CC PRODUCED BY ALTERNATIVE SPlicing.
 CC -I- DOMAIN: THE REPEATED DOMAIN Binds TO TUBULIN.
 CC -I- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
 DR PIR; JS0306; JS0306.
 DR A33574; A33574.
 DR PFAM; PF00418; tubulin-binding; 4.
 DR PROSITE; PS00229; TAU_MAP1; 4.
 KW MICROTUBULES; Repeat; Alternative splicing; Phosphorylation.
 FT REPEAT 235 265 TAU/MAP MOTIF.
 FT REPEAT 266 296 TAU/MAP MOTIF.
 FT REPEAT 297 327 TAU/MAP MOTIF.
 FT REPEAT 328 359 TAU/MAP MOTIF.
 FT DISULFID 282 313 BY SIMILARITY.
 FT MOD_RES 347 347 PROSPHORYLATION (BY CAPK1) (POTENTIAL).
 FT VARSPICE 266 296 MISSING (IN FETAL ISOFORM).
 FT VARSPICE 275 305 MISSING (IN ISOFORM 1 AND ISOFORM 3).
 FT VARSPICE 275 305 MISSING (IN ISOFORM 2 AND ISOFORM 3).
 FT VARSPICE 1 44 MAERQEEFEMDHAFTGTYGIGDRKQDGHHQHODDEGDTDA GLR -> MRLQQRK (IN FETAL ISOFORM).
 FT VARSPICE 278 308 MISSING (IN FETAL ISOFORM).
 SQ SEQUENCE 441 AA: 45580 MW: 835A8706DB847A8CC CRC64;

 Query Match 93.5%; Score 58; DB 1; length 441;
 Best Local Similarity 83.3%; Pred. No. 0.019; 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Gaps 0;
 ID TAU_HUMAN STANDARD; PRD; 441 AA.
 AC P10536; P10518; Q14799; Q15551;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN TAU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE; 93041757.
 RA Andreais A.; Brown W.M.; Kosik K.S.;
 RT "Structure and novel exons of the human tau gene."; Biochemistry 31:10626-10633(1992).
 RL [2] SEQUENCE FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 89351564.
 RA Goedert M.; Spillantini M.G.; Potier M.C.; Ulrich J.; Crowther R.A.;
 RT "Cloning and sequencing of the cDNA encoding an isoform of microtubule-associated protein tau containing four tandem repeats: differential expression of tau protein mRNAs in human brain."; EMBO J. 8:393-399(1989).
 RL [3] SEQUENCE OF 1-26 AND 306-441 FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 88034557.
 RA Goedert M.; Wischik C.; Crowther R.; Walker J.; Klug A.;
 RT "Cloning and sequencing of the cDNA encoding a core protein of the paired helical filament of Alzheimer disease: identification as the microtubule-associated protein tau"; Proc. Natl. Acad. Sci. U.S.A. 85:4051-4055(1988).
 RL [4] SEQUENCE OF 1-26 AND 306-441 FROM N.A.
 RC TISSUE-BRAIN.
 RX MEDLINE; 90180482.

 Lee G.; Neve R.L.; Kosik K.S.; "The microtubule binding domain of tau protein." ; Neuron 2:1161-1164(1989).
 RL J. Cell Biol. 109:1173-1184(1989);
 CC 1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
 CC MICROTUBULES.
 CC -I- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
 CC PRODUCED BY ALTERNATIVE SPlicing.
 CC -I- DOMAIN: THE REPEATED DOMAIN Binds TO TUBULIN.
 CC -I- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
 DR PIR; JS0306; JS0306.
 DR A33574; A33574.
 DR PFAM; PF00418; tubulin-binding; 4.
 DR PROSITE; PS00229; TAU_MAP1; 4.
 KW MICROTUBULES; Repeat; Alternative splicing; Phosphorylation.
 FT REPEAT 235 265 TAU/MAP MOTIF.
 FT REPEAT 266 296 TAU/MAP MOTIF.
 FT REPEAT 297 327 TAU/MAP MOTIF.
 FT REPEAT 328 359 TAU/MAP MOTIF.
 FT DISULFID 282 313 BY SIMILARITY.
 FT MOD_RES 347 347 PROSPHORYLATION (BY CAPK1) (POTENTIAL).
 FT VARSPICE 266 296 MISSING (IN FETAL ISOFORM).
 FT VARSPICE 275 305 MISSING (IN ISOFORM 1 AND ISOFORM 3).
 FT VARSPICE 275 305 MISSING (IN ISOFORM 2 AND ISOFORM 3).
 FT VARSPICE 1 44 MAERQEEFEMDHAFTGTYGIGDRKQDGHHQHODDEGDTDA GLR -> MRLQQRK (IN FETAL ISOFORM).
 FT VARSPICE 278 308 MISSING (IN FETAL ISOFORM).
 SQ SEQUENCE 441 AA: 45580 MW: 835A8706DB847A8CC CRC64;

RESULT 6
 TAUL_BOVIN STANDARD; PRT; 448 AA.
 AC P29172; (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DT 15-JUL-1998 (Rel. 37, Last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN TAU FORMS 1 AND 2.
 GN MAP.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89261765.
 RA Hämmerl A., Drechsler D., Kirschner M.W., Martin D.W. JR.;
 RT "Tau consists of a set of proteins with repeated C-terminal microtubule-binding domains and variable N-terminal domains.";
 RL Mol. Cell. Biol. 9:1381-1388(1989).
 CC MICROTUBULES.
 CC -!- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- DOMAIN: THE REPEATED DOMAIN Binds TO TUBULIN.
 CC -!- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED BY CAMP KINASE.
 CC -!- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
 CC
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 CC
 CC
 DR EMBL: L34953; AAA51609_1; -.
 DR EMBL: L34940; AAA51609_1; JOINED.
 DR EMBL: L34941; AAA51609_1; JOINED.
 DR EMBL: L34942; AAA51609_1; JOINED.
 DR EMBL: L34943; AAA51609_1; JOINED.
 DR EMBL: L34944; AAA51609_1; JOINED.
 DR EMBL: L34945; AAA51609_1; JOINED.
 DR EMBL: L34947; AAA51609_1; JOINED.
 DR EMBL: L34948; AAA51609_1; JOINED.
 DR EMBL: L34949; AAA51609_1; JOINED.
 DR EMBL: L34950; AAA51609_1; JOINED.
 DR EMBL: L34951; AAA51609_1; JOINED.
 DR EMBL: M06157; AAA50770_1; -.
 DR PIR: A31939; Q8B0T1.
 DR PROSITE: PS00418; tubulin-binding; 4.
 KW Microtubules; Repeat; Alternative splicing.
 FT REPEAT 251 281 TAU/MAP MOTIF.
 FT REPEAT 282 312 TAU/MAP MOTIF.
 FT REPEAT 313 343 TAU/MAP MOTIF.
 FT REPEAT 344 375 MISSING (IN ISOFORM 2).
 FT VARSPLC 175 192 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 448 AA: 46332 MW: 821638A9C4809602 CRC64;

Query Match 93.5%; Score 58; DB 1; Length 448;
 Best Local Similarity 83.3%; Pred. No. 0.02;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGVSSXPSPGT 12
 Db 201 RSGVSSPSPGT 212

RESULT 7
 WA_EMENT ID WA_EMENT STANDARD; PRT; 1986 AA.
 AC 003149;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CONIDIAL GREEN PIGMENT SYNTHASE (EC 2.3.1.-).
 GN EMERICELLA nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Eurotiomycetes; Emericella.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93101122.
 RA Mayorga M.E., Timberlake W.E.;
 RT "The developmentally regulated Aspergillus nidulans wa gene encodes a polypeptide homologous to Polyketide and fatty acid synthases.";
 RL Mol. Genet. 235:205-212(1992).
 CC -!- FUNCTION: THIS PROTEIN CONDENSES CARBON UNITS TO FORM AN INTERMEDIATE YELLOW POLYKETIDE PIGMENT THAT IS POLIMERIZED BY CONIDIAL LACCASE TO FORM THE GREEN PIGMENT IN MATURE
 CC -!- ASEXUAL SPORES (CONIDIA).
 CC -!- COFACTOR: CONTAINS 2 COVALENTLY BOUND PHOSPHOPANTETHINES (POENTIAL).
 CC -!- PATHWAY: BIOSYNTHESIS OF CONIDIAL GREEN PIGMENT.
 CC -!- SIMILARITY: WITH BOTH EUKARYOTIC AND PROKARYOTIC POLYKETIDE
 CC -!- SYNTHASES AND VERBERATE FATTY ACID SYNTHASES.
 CC
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 CC
 DR EMBL: X65866; CAH46695_1; -.
 DR PIR: S28353; S28353.
 DR PFAM: PF00698; Acyl transf; 1.
 DR PFAM: PF00109; ketoacyl synth; 1.
 DR PFAM: PF00550; PP-binding; 2.
 DR PROSITE: PS00012; PHOSPHOPANTETHINE; 1.
 DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; 1.
 DR PROSITE: PS0075; ACP_DOMAIN; 2.
 KW Transf erase; Phosphopantetheine; Multifunctional enzyme.
 FT DOMAIN 529 582 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
 FT DOMAIN 991 1024 ACYL/MALONYL TRANSFERASES (BY SIMILARITY).
 FT DOMAIN 1650 1719 ACYL CARRIER (ACP).
 FT DOMAIN 1772 1841 ACYL CARRIER (ACP).
 FT ACT_SITE 548 548 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
 FT ACT_SITE 1001 1001 ACYL/MALONYL TRANSFERASES (BY SIMILARITY).
 FT BINDING 1682 1682 PHOSPHOPANTETHINE (BY SIMILARITY).
 FT BINDING 1804 1804 PHOSPHOPANTETHENE (BY SIMILARITY).
 SQ SEQUENCE 1986 AA: 216364 MW: 744F0940FF40EE9A CRC64;

RESULT 8
 SYM_PODAN ID SYM_PODAN STANDARD; PRT; 640 AA.
 AC P28659;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)

RT "Cloning of the human and mouse type X collagen genes and mapping of the mouse type X collagen gene to chromosome 10.";
 RT Bur. J. Biochem. 206:217-224(1992).
 RL [4]
 RN SEQUENCE OF 385-627 FROM N.A.
 RC STRAIN=CBBL;
 RX MEDLINE; 92182017.
 RA Elina K., Metsaeranta M., Kallio J., Peraelae M., Ferola I.,
 RA Garofalo S., de Crombrugge B., Vuorio E.;
 RT "Specific hybridization probes for mouse alpha 2(IX) and alpha 1(X)
 RT collagen mRNAs.";
 RL BLOCHI. BIOPHYS. Acta 1130:78-80(1992).
 CC -!- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
 CC -!- SUBUNIT: HOMOTIMER.
 CC -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPÉPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
 CC -!- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
 CC -!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.

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DR EMBL; X07348; CARMT763_1; -.
 DR EMBL; X05121; CAA6237_1; -.
 DR EMBL; X23013; CAA4741_1; -.
 DR EMBL; Z21610; CAA79736_1; -.
 DR PIR; S28807; S28807.
 DR PROSITE; PS01113; C1Q; 1.
 DR PRINTS; PRO0007; COMPLEMENTC1Q.
 DR PRINTS; PRO00386; C1Q; 1.
 DR PIR; S31216; S31216.
 DR PIR; S22215; S22215.
 DR MGDB; 88445; COL10A1.
 DR PFAM; PF001391; Collagen; 6.
 DR PROSITE; PS01113; C1Q; 1.
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Cartilage; Collagen; Signal; Potential.

FT SIGNAL 1 18
 FT CHAIN 19 680
 FT DOMAIN 19 56
 FT DOMAIN 57 519
 FT DOMAIN 520 680
 FT DOMAIN 545 680
 FT CONFLICT 248 248
 FT CONFLICT 286 286
 FT CONFLICT 306 306
 FT CONFLICT 417 417
 FT CONFLICT 451 451
 FT CONFLICT 500 500
 FT CONFLICT 567 567
 FT CONFLICT 569 569
 FT CONFLICT 571 572
 FT CONFLICT 635 635
 SQ SEQUENCE 580 AA; 56775 MW; FE984C99A708E2 CRC64;

Query Match 64.5%; Score 40; DB 1; Length 680;
 Best Local Similarity 54.5%; Pred. No. 24; Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KGSYSXGSPG 11
 ::||| ||| |||
 Db 190 ENGGSPGRPG 200

ID PIP6_HUMAN STANDARD; PRT; 756 AA.
 ID AC P01178;
 ID DT 01-OCT-1996 (Rel. 34, Created)
 ID DT 01-OCT-1996 (Rel. 34, Last sequence update)
 ID DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODISTERASE DELTA 1.
 DE (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE CDELTA-1) (PLC-III).
 GN PLC1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-NORTA;
 RX MEDLINE; 95197554.
 RA Cheng H.F., Jiang M.J., Chen C.L., Liu S.M., Wong L.P.,
 RA Lomasney J.W., King K.;
 RA "Cloning and identification of amino acid residues of human phospholipase C delta 1 essential for catalysis.";
 RA J. Biol. Chem. 270:5495-5505(1995).
 CC -!- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C ENZYMES.

CC -!- CATALYTIC ACTIVITY: 1-PHOSPHATIDYL-D-MYO-INOSITOL 4,5-BISPHOSPHATE + H(2)O = D-MYO-INOSITOL 1,4,5-TRIPHOSPHATE + DIACYLGLYCEROL.

CC -!- COFACTOR: REQUIRES CALCIUM.

CC -!- MICELLATION: THERE ARE AT LEAST SIX FORMS OF PLC ENZYMES.

CC -!- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.

CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.

CC -!- SIMILARITY: CONTAINS 2 EF HAND CALCIUM-BINDING DOMAINS.

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CC DR EMBL; U09117; AAA73567_1; -.
 CC DR HSSP; P1068B; IMAI.
 CC DR XM; 602142; -.
 CC DR PFAM; PF00168; C2; 1.
 CC DR PFAM; PF00169; PH; 1.
 CC DR PFAM; PF00388; PI-PIC-X; 1.
 CC DR PFAM; PF00387; PI-PIC-Y; 1.
 CC DR PFAM; PF00336; ephand; 1.
 CC DR PRINTS; PRO0360; C2DOMAIN.
 CC DR PRINTS; PRO0390; PHPIPIPASEC.
 CC DR PROSITE; PS00018; EF_HAND; 2.
 CC DR PROSITE; PS50003; PH_DOMAIN; 1.
 CC DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 CC DR PROSITE; PS50007; PIPLIC_X_DOMAIN; 1.
 CC DR PROSITE; PS50008; PIPLIC_Y_DOMAIN; 1.
 KW Hydrolase; Lipid degradation; Transducer; Calcium-binding.
 FT DOMAIN 2 1 130
 FT CAL_BIND 153 164 SITE 1 (POTENTIAL).
 FT CAL_BIND 189 200 SITE 2 (POTENTIAL).
 FT DOMAIN 296 440 DOMAIN X.
 FT DOMAIN 492 609 DOMAIN Y.
 FT ACT_SITE 616 720 C2 DOMAIN.
 FT ACT_SITE 311 311 BY SIMILARITY.
 SQ SEQUENCE 756 AA; 85763 MW; ADDA4251C5EBADFB CRC64;

Query Match 64.5%; Score 40; DB 1; Length 756;
 Best Local Similarity 66.7%; Pred. No. 27; Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 11
 PIP6_HUMAN

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CC EMBL: X56579; CAA40299.1; -;
CC DR EMBL: Z27078; CAA81584.1; -;
CC DR EMBL: J05067; RAB59179.1; -;
CC DR PIR: B34476; B34476.
DR WORMEP; R04H4.1; CB00246.
DR PFAM: PF01413; C4; 2.
DR PFAM: PF01391; Collagen; 22.
KW Extracellular matrix; Connective tissue; Basement membrane;
Repeat; Hydropxylase; Glycoprotein; Collagen; Signal;
FT SIGNAL 1
FT PROPEP ? 2194 AMINO TERMINAL PROPEPTIDE (7S DOMAIN).
FT CHAIN ? 195 COLLAGEN ALPHA 1(IV) CHAIN.
FT DOMAIN 195 TRIPLE-HELICAL REGION.
FT DOMAIN 1530 NONHELICAL REGION (NCL).
FT DISULFID 1549 OR 1637 (BY SIMILARITY).
FT DISULFID 1582 OR 1640 (BY SIMILARITY).
FT DISULFID 1594 BY SIMILARITY.
FT DISULFID 1659 OR 1751 (BY SIMILARITY).
FT DISULFID 1693 OR 1754 (BY SIMILARITY).
FT DISULFID 1705 BY SIMILARITY.
FT VARIANT 402 G -> E (IN MUTANT G34).
FT VARIANT 408 G -> E (IN MUTANT G23/HC70).
FT CONFLICT 1514 P -> Q (IN REF. 3).
FT CONFLICT 130 PVGPA -> LSDQLY (IN REF. 2).
FT CONFLICT 259 KGGKGRSGRSGVGPGL -> VSDLSKSDCINTIHSIDVS
FT CONFLICT 304 KDAKEKENEDQEQQVQ (IN REF. 2).
FT CONFLICT 304 LDN -> AGQR (IN REF. 2).
FT CONFLICT 366 MISSING ((IN REF. 2)).
FT CONFLICT 581 G -> R (IN REF. 2).
FT CONFLICT 768 P -> R (IN REF. 2).
FT CONFLICT 813 PG -> TR (IN REF. 2).
FT CONFLICT 830 D -> V (IN REF. 2).
FT CONFLICT 1275 P -> T (IN REF. 2).
FT CONFLICT 1722 P -> L (IN REF. 2).
FT SEQUENCE 1758 AA; 170857 MW; 7083D9AF63E05D45 CRC64;

Query Match 64.5%; Score 40; DB 1; Length 1758;
Best Local Similarity 66.7%; Prid. 62%;
Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;
Qy 1 KSGYSXPGPCT 12
Db 1474 KASGY--PGAPGT 1483

RESULT 14
CA24-CAEEL STANDARD; PRT; 1758 AA.

CA24-CAEEL STANDARD; PRT; 1758 AA.

AC P17440;
DT 01-OCT-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 30, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE COLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.
GN LET-2 OR CIB-1.
OS Caenorhabditis elegans.
OC Rhabditida; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderrinae; Caenorhabditis.
RN [1]
SEQUENCE FROM N A
STRAIN-BRISTOL N2;
MEDLINE: 94012964.
RA Sibley M H.; Johnson J.J.; Mello C.C.; Kramer J.M.;
"Genetic identification, sequence, and alternative splicing of the

RT Caenorhabditis elegans alpha 2(IV) collagen gene.";
RL J. Cell Biol. 123:255-264(1993).
RN [2]
RT PRELIMINARY SEQUENCE OF 1495-1758 FROM N.A.
RP STRAIN-BRISTOL N2;
RC MEDLINE: 9006929.
RN Guo X.; Kramer J.M.;
"The two *Caenorhabditis elegans* basement membrane (type IV) collagen genes are located on separate chromosomes.";
RT J. Biol. Chem. 264:17574-17582(1989).
RN [3]
RP MEDLINE: 94320591.
RA Sibley M.H.; Graham P.L.; von Meude N.; Kramer J.M.;
"Mutations in the alpha 2(IV) basement membrane collagen gene of *Caenorhabditis elegans* produce phenotypes of differing severities.";
RT EMBO J. 13:3778-3785(1994).
CC -1- FUNCTION: COLLAGEN TYPE IV IS SPECIFIC FOR BASEMENT MEMBRANES.
CC -1- SUBUNIT: TRIMERS OF TWO ALPHA 1(IV) CHAIN.
CC -1- TYPE IV COLLAGEN FORMS A MESH-LIKE NETWORK LINKED THROUGH
INTERMOLECULAR INTERACTIONS BETWEEN 7S DOMAINS AND BETWEEN NCL
DOMAINS.
CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS; I (SHOWN HERE) AND II; ARE
PRODUCED BY ALTERNATIVE SPlicing.
CC -1- TISSUE SPECIFICITY: FORM I IS PREDOMINANT IN EMBRYOS AND FORM
II IS PREDOMINANT IN THE LARVAE AND ADULTS.
CC -1- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
DOMAIN (NCL) AT THEIR C-TERMINUS; FREQUENT INTERRUPTIONS OF THE
G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
CAUSE FLEXIBILITY IN THE TRIPLE HELIX) AND A SHORT N-TERMINAL
TRIPLE-HELICAL 7S DOMAIN.
CC -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPPLETIDE REPEATING
UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1- PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH
ARE INVOLVED IN INTR- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF
THESE, LOCATED IN THE NCL DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
IV COLLAGENS.
CC -1- DISEASE: MUTATIONS IN LET-2 ARE GENERALLY EMBRYONIC LETHAL.

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CC DR EMBL: Z22954; CAA80535.1; -;
CC DR EMBL: Z22964; CAA80537.1; -;
CC DR EMBL: J05066; AAA27989.1; -;
CC DR EMBL: U2327; AA6464312.1; ALT_SEQ.
CC DR PIR: A34476; A34476.
CC DR PFAM: PF01413; C4; 2.
CC DR PFAM: PF01391; Collagen; 23.
KW Hydroxylation; Connective tissue; Basement membrane; Repeat; Collagen;
KW Hydroylation; Connective tissue; Basement membrane; Repeat; Collagen;
KW Alternative splicing; Glycoprotein; Signal.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 1758 COLLAGEN ALPHA 2(IV) CHAIN.
FT DOMAIN 27 42 7S DOMAIN.
FT DOMAIN 42 1527 TRIPLE-HELICAL REGION.
FT DOMAIN 1528 1758 NONHELICAL REGION (NCL).
FT DISULFID 1546 1635 OR 1632 (BY SIMILARITY).
FT DISULFID 1579 1632 OR 1635 (BY SIMILARITY).
FT DISULFID 1591 1597 BY SIMILARITY.
FT DISULFID 1654 1750 OR 1747 (BY SIMILARITY).
FT DISULFID 1688 1747 OR 1750 (BY SIMILARITY).
FT DISULFID 1700 1707 BY SIMILARITY.
FT CARBOHYD 248 O-LINKED (GLUCOSAMINOGLYCAN) (POTENTIAL).
FT VARIANT 48 48 G -> E (IN MN114; 73% LETHAL).
FT VARIANT 366 366 A -> T (IN MN116; 100% LETHAL).
FT VARIANT 570 570 G -> E (IN MN109; 37% LETHAL).
FT VARIANT 588 588 G -> R (IN MN103 AND MN111; 96% LETHAL).
FT VARIANT 597 597 G -> R (IN MN152; 50% LETHAL).

FT VARIANT 690 690 G -> R (IN MN101; 100% LETHAL).
 FT VARIANT 690 690 G -> E (IN MN129; 100% LETHAL).
 FT VARIANT 737 737 G -> E (IN MN113; 100% LETHAL).
 FT VARIANT 877 877 G -> R (IN G30; 90% LETHAL).
 FT VARIANT 904 904 G -> R (IN E1140; 94% LETHAL).
 FT VARIANT 1003 1003 G -> E (IN MN139; 20% LETHAL).
 FT VARIANT 1125 1125 G -> D (IN G25; 2% LETHAL).
 FT VARIANT 1152 1152 G -> D (IN MN147; 7% LETHAL).
 FT VARIANT 1286 1286 G -> D (IN G37 AND B246; 9% LETHAL).
 FT VARSPIC 229 264 GDLGSVGGPGPGRPTGGGSIVGGRNGEKGDK -> G
 DIGAMKPGAGPGPLASTMSRGTLGPKGDIGEGEK (IN ISOFORM II).

PT CONFLICT 1682 1682 P -> L (IN REF. 1). CRC54;
 SQ SEQUENCE 1758 AA; 167750 MW; 97EE3F3DBB2D2AC5

Query Match Similarity 64.5%; Score 40; DB 1; Length 1758;
 Best Local Similarity 54.5%; Pred. No. 62;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 KSGYSXPSPG 11
 ::||| |||||
 Db 680 EAGYSOPGPQG 690

RESULT 15
 ACCC_ANASP STANDARD; PRT; 447 AA.
 AC 006862;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE BIOTIN CARBOXYLASE (EC 6.3.4.14) (A SUBUNIT OF ACETYL-COA
 DE CARBOXYLASE (EC 6.4.1.2)) (ACCI).
 GN ACCC.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93352435.
 RA Gornicki P., Scappino L.A., Haselkorn R.;
 RT "Genes for two subunits of acetyl coenzyme A carboxylase of Anabaena
 sp. strain PCC 7120: biotin carboxyl carrier
 protein.";
 RL J. Bacteriol. 175:568-572(1993).
 CC -I- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A
 CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE
 CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSACARBOXYLASE
 TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA.
 CC -I- CATALYTIC ACTIVITY: ATP + BIOTIN-CARBOXYL-CARRIER PROTEIN + CO(2)
 = ADP + ORTHOBOSPHATE + CARBOXYBIOTIN-CARBOXYL-CARRIER PROTEIN.
 CC -I- PATHWAY: FIRST STEP IN LONG-CHAIN FATTY ACID SYNTHESIS.
 CC -I- SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN
 CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS
 OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX.
 CC -I- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBAMOYL-
 PHOSPHATE SYNTHASES.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@ibb-sib.ch).

CC EMBL; Li4862; AAB51770.1; -.
 DR BNSP; P24102; IBNC.
 DR PPAM; PF0089; CPSase_L-chain; 1.
 DR PROS1; PS00866; CPSase_1.
 DR PROS1; PS00867; CPSase_2; 1.
 KW Fatty acid biosynthesis; Ligase; Biotin; ATP-binding.
 KW MP_BIND 163 168 ATP (BY SIMILARITY).

FT ACT-SITE 293 293 BY SIMILARITY
 SEQUENCE 447 AA; 49104 MW; 8A541B38B39E00F9 CRC64;
 SQ

Query Match Similarity	Score	DB	Length	Indels	Gaps
63.9%	39	1	447	0	0
Best Local Similarity	70.0%	Pred. No.	23	3	0
Matches	7;	Conservative	0;	Mismatches	
Qy	2 SGYSXPSPG 11	Db	357 SGYLPGGPG 366		

Search completed: October 2, 2000, 18:43:36
 Job time: 2483 sec

Tue Oct 3 09:21:59 2000

us-09-142-613-2.rsp

Page 10

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: October 2, 2000, 17:34:39 ; Search time 162.96 Seconds
(without alignments) updates/sec

Title: US-09-142-613-2
Perfect score: 62
Sequence: 1 KSGYSWPGSPGT 12

Scoring table: BLOSUM62
Gpop 10.0 , Gapext. 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL_12:
1: sp_archeal:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_micr:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_ricket:
12: sp_virus:
13: sp_vertebrat:
14: sp_unclassified:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Description	RESULT	1	ALIGNMENTS
1	58	93.5	Q28189 bos taurus	Q28189	PRELIMINARY;	
2	58	93.5	Q28190 bos taurus	Q28189	PRT;	316 AA.
3	58	93.5	Q28188 bos taurus	Q28189;		
4	58	93.5	Q28186 mus musculus	DT	01-NOV-1996 (TREMBrel. 01, Created)	
5	58	93.5	Q28186 bos taurus	DT	01-NOV-1996 (TREMBrel. 01, Last sequence update)	
6	58	93.5	Q28185 bos taurus	DT	01-NOV-1999 (TREMBrel. 12, Last annotation update)	
7	58	93.5	Q28185 mus musculus	DE	TAU PROTEIN.	
8	58	93.5	Q28185 mus musculus	GN	TAU	
9	58	93.5	Q28185 bos taurus	OS	Bos taurus (Bovine). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; OC	
10	58	93.5	Q28185 bos taurus	OC	Bovinae; Bos.	
11	58	93.5	Q28185 bos taurus	RN	[1]	
12	58	93.5	Q28185 bos taurus	RX	SEQUENCE FROM N.A.	
13	58	93.5	Q28185 bos taurus	RA	HIMMELER A., DRECHER D., KIRSCHNER M.W., MARTIN D.W.; "Tau consists of a set of proteins with repeated C-terminal microtubule-binding domains and variable N-terminal domains."; Mol. Cell. Biol. 9:1381-1388(1989).	
14	58	93.5	Q28185 bos taurus	RN	[2]	
15	58	93.5	Q28185 bos taurus	RP	SEQUENCE FROM N.A.	
16	58	93.5	Q28185 bos taurus	RX	HIMMELER A.;	
17	58	93.5	Q28185 bos taurus	RA	"Structure of the bovine tau gene: alternatively spliced transcripts generate a protein family."; Mol. Cell. Biol. 9:1389-1396(1989).	
18	58	93.5	Q28185 bos taurus	RT	MOL: M26178; AAC51606.1; -	
19	58	93.5	Q28185 bos taurus	DR	EMBL: L44940; AAC51606.1; JOINED.	
20	58	93.5	Q28185 bos taurus	DR	EMBL: L44941; AAC51606.1; JOINED.	
21	58	93.5	Q28185 bos taurus	DR	EMBL: L44942; AAC51606.1; JOINED.	
22	58	93.5	Q28185 bos taurus	DR	EMBL: L44943; AAC51606.1; JOINED.	
23	58	93.5	Q28185 bos taurus	DR	EMBL: L44945; AAC51606.1; JOINED.	
24	58	93.5	Q28185 bos taurus	DR	EMBL: L44946; AAC51606.1; JOINED.	
25	58	93.5	Q28185 bos taurus	DR	EMBL: L44948; AAC51606.1; JOINED.	
26	58	93.5	Q28185 bos taurus	DR	EMBL: L44950; AAC51606.1; JOINED.	
27	58	93.5	Q28185 bos taurus	DR	EMBL: L44951; AAC51606.1; JOINED.	
28	58	93.5	Q28185 bos taurus	DR	PROSITE: PS00229; TAU_MAP; 3.	
29	58	93.5	Q28185 bos taurus	DR	PF00418; tubulin-binding; 3.	
30	58	93.5	Q28185 bos taurus	KW	Microtubules; Repeat.	
31	58	93.5	Q28185 bos taurus	SEQUENCE	316 AA; 32770 MN; DBC3A429 CRC32;	
32	58	93.5	Q28185 bos taurus	Query Match	93.5%; Score 58; DB 6; Length 316;	

Db	201	RSGYSSPGSPGT	212	ID	Q17939	PRELIMINARY;	PRT;	295 AA.
ID	060684			AC	Q17939;			
AC	060684;			DT	01-NOV-1996 (TREMBREL 01, Created)			
DT	01-NOV-1996 (TREMBREL 01, Last sequence update)			DT	01-NOV-1996 (TREMBREL 01, Last sequence update)			
DT	01-NOV-1999 (TREMBREL 12, Last annotation update)			DE	C12D8.9 PROTEIN.			
DE	NICROBUBBLE-ASSOCIATED PROTEIN TAU ISOFORM 23.			GN	C12D8.8.			
OS	Mus musculus (Mouse);			CAenorhabditis elegans.				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			OC	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;			
OC	Butharia; Rodentia; Sciurognathii; Muridae; Murinae; Mus.			OC	Rhabditina; Rhabditioidea; Peioderinae; Caenorhabditis.			
RN	[1]			RN	[1]			
RP	SEQUENCE FROM N.A.			SEQUENCE FROM N.A.				
RA	STRAIN=HIM OFI spp.; TISSUE=LIVER;			RA	WILSON R., ATNSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,			
RA	KENNER L., EFERL R., ZATKOVSKA K., HOEFFLER G., DENK H.,			RA	BONFIELD J., BURTON J., CONNELL M., COPSET T., COOPER J., COULISON A.,			
RL	Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.			RA	CRAXTON M., DEAR S., DU Z., DURBIN R., FAYELO A., FULTON L.,			
DR	EMBL: U10314; ARAS8243.1; -.			RA	GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,			
DR	PROSITE; PS00239; TAU_MAP; 4.			RA	JONES M., KERSHAW J., KIRSTEN J., LATISTER N., LATREILLE P.,			
DR	PFAM; PF00418; tubulin-binding; 4.			RA	LIGHTNING J., LLOYD C., MCMURRAY A., MORTMORE B., O'CALLAGHAN M.,			
RW	Microtubules; Repeat; RIFKEN A., ROOPRA A., SAUNDERS D., SHONKEEN R.,			RA	PARSONS J., PERCY C., RIFKEN A., SONNHAMMER E., STADEN R., SULSTON J.,			
SEQUENCE	430 AA; 44893 MW; FD52F55A CRC32;			RA	SMALDON N., SMITH A., SONNHAMMER E., SULSTON J., THERRY MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSON R.,			
Query Match	93.5%; Score 58; DB 11; Length 430;			RA	WATSON A., WEINSTOCK L., WILKINSON-SRROAT J., WOHLDAHN P.,			
Best Local Similarity	83.3%; Pred. No. 0.019;			RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans";			
Matches	10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			RL	Nature 368:332-38(1994); EMBL: Z73969; CAA8236; 1; -.			
QY	1 KSGYSSPGSPGT 12			DR	DR			
Db	183 RSGYSSPGSPGT 194			DR	PFAM; PF011484; Col_cuticle_N; 1.			
SQ	SEQUENCE 295 AA; 30342 MW; 26A15EF5 CRC32;			DR	SEQUENCE 295 AA; 30342 MW; 26A15EF5 CRC32;			
RESULT	12			Query Match	71.0%; Score 44; DB 5; Length 295;			
063567				Best Local Similarity	63.6%; Pred. No 3.2;			
ID	063567	PRELIMINARY;	PRT;	Matches	7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;			
AC	063567;			QY	1 KSGYSSPGSPGT 11			
DT	01-NOV-1996 (TREMBREL 01, Created)			Db	213 KRSGYGPAGP 223			
DT	01-NOV-1996 (TREMBREL 01, Last sequence update)							
DT	01-NOV-1999 (TREMBREL 12, Last annotation update)							
DE	BIG TAU.							
GN	TAU.							
OS	Rattus norvegicus (Rat).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;							
OC	Eutheria; Rodentia; Sciuromorphati; Muridae; Murinae; Rattus.							
RN	[1]	SEQUENCE FROM N.A.						
RP	MEDLINE: 92179305.							
RX	GOEDERT M., SPILLANTINI M.G., CROWTHER R.A.;							
RT	*Cloning of a big tau microtubule-associated protein characteristic of the peripheral nervous system"; 89:1983-1987(1992).							
RT	Proc. Natl. Acad. Sci. U.S.A. 89:1983-1987(1992).							
RL	EMBL: M84156; AAA42204.1; -.							
DR	PS00229; TAU_MAP; 4.							
DR	PFAM; PF00418; tubulin-binding; 4.							
RW	Microtubules; Repeat; SEQUENCE 686 AA; 71774 MW; 70992021 CRC32;							
SQ	SEQUENCE 686 AA; 71774 MW; 70992021 CRC32;							
Query Match	93.5%; Score 58; DB 11; Length 686;							
Best Local Similarity	83.3%; Pred. No. 0.031; 1; Indels 0; Gaps 0;							
Matches	10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;							
QY	1 KSGYSSPGSPGT 12							
QY	:							
Db	439 RSGYSSPGSPGT 450							
RESULT	13							
017939	SEQUENCE FROM N.A.							

Search completed: October 2, 2000, 18:16:47
 Job time: 2528 sec

RC STRAIN-DL G109;
 RX MEDLINE: 96250169;
 RA FERRER P., HEDEGAARD L., HALKIER T., DIERS I., SAVVA D., ASENJO J.-A.;
 RT "Molecular cloning of a lytic beta-1,3-glucanase gene from Oeiskovia
 RT xanthineolytica LG109. A beta-1,3-glucanase able to selectively
 RT permeabilize the yeast cell wall";
 RL Ann. N. Y. Acad. Sci. 782:555-566(1996).
 RN [4]
 RP SEQUENCE FROM N. A.
 RC STRAIN-DL G109;
 RA FERRER P., ANDRENS B.A., ASENJO J.A., HEDEGAARD L., DIERS I.;
 RL Submitted (MAR 1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF052145; AAC38290.1; -;
 DR HSSP; P23904; IAKR.
 DR PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
 DR PFAM; PF00652; Ricin_B_lectin; 1.
 SQ SEQUENCE 435 AA; 46097 MW; B7C717E CRC32;

Query Match 69.4%; Score 43; DB 5; Length 553;
 Best Local Similarity 72.7%; Pred. No. 9; 2;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 SGYSXPGSPGT 12
 Db 323 SGFSTPGSPFT 333

RESULT 15
 093367 PRELIMINARY;
 ID 093367; PRT; 553 AA.
 AC 093367;
 DT 01-FEB-1997 (TREMBREL. 02, Created)
 DT 01-JAN-1998 (TREMBREL. 05, Last sequence update)
 DT 01-JAN-1999 (TREMBREL. 09, Last annotation update)
 DE C41G7.3 PROTEIN
 GN C41G7.3
 OS Caenorhabditis elegans
 OC Rhabditina; Metacoea; Secernentea; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Pelerinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N. A.
 RA STEWARD C.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N. A.
 RX MEDLINE;
 RX 94150718.
 WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COOPER J., COULSON A.,
 BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 CRAXTON M., DEAR S., DU Z., DUBIN R., FAVELLO A., FULTON L.,
 GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LARVILLE P.,
 LIGHTING J., LLOYD C., MCMURRAY A., MORTMORE B., O'CALLAGHAN M.,
 PARSONS J., PERCY C., RIFKEN A., ROOPRA A., SHONKEEN R.,
 SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 WATSON A., WEINSTOCK L., WILKINSON-SPROAT P., WOHLMAN P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-33(1994).
 DR EMBL; Z81048; CAB02840.1; -;
 SQ SEQUENCE 553 AA; 61142 MW; A2548F6C CRC32;

Query Match 69.4%; Score 43; DB 5; Length 553;
 Best Local Similarity 72.7%; Pred. No. 9; 2;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Tue Oct 3 09:22:00 2000

us-09-142-613-2.rspt

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OM protein - protein search, using sw model

Title: US-09-142-613-2
Perfect score: 62

Sequence: 1 KSGYSXPGSPGT 12

Scoring table:
BLOSUM62
Gappen 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36,*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	98.4	12	1 W34857	Human tau protein
2	58	93.5	34	1 R61330	Peptide Phosphoryl Human tau protein
3	58	93.5	34	1 W34875	Human tau protein
4	58	93.5	67	1 R59837	Sequence of human Microtubule-associa
5	58	93.5	106	1 R92516	PHF-tau (143-254)
6	58	93.5	112	1 R76937	Paired helical fil
7	58	93.5	352	1 P91294	Paired helical fil
8	58	93.5	352	1 R32708	Human tau-protein.
9	58	93.5	390	1 W05283	Truncated human ta
10	58	93.5	441	1 R58810	Human tau protein.
11	58	93.5	441	1 W05282	Human tau protein.
12	58	93.5	441	1 W34856	Human tau protein.
13	46	74.2	9	1 R36557	Peptide sequence
14	46	74.2	12	1 R38235	Alzheimer paired h
15	46	74.2	12	1 R37554	Phosphorylated tau
16	44	71.0	263	1 W29455	Oerskovia xanthine
17	44	71.0	435	1 W29456	Oerskovia xanthine
18	39	62.9	13	1 R28237	Phosphopeptide as
19	39	62.9	13	1 W34860	Human tau protein
20	39	62.9	13	1 W34858	Human tau protein
21	39	62.9	234	1 W53973	Pseudomonas fluores
22	39	62.9	303	1 W29457	Oerskovia xanthine
23	39	62.9	447	1 W05207	Anabena biotin bi
24	39	62.9	447	1 W70402	Anabena biotin bi
25	39	62.9	448	1 R31080	Biotin carboxylase.
26	38	61.3	1 R87998	Subtilisin 309 lco	
27	38	61.3	286	1 R23924	blac74 mutation (8
28	38	61.3	1 W70515	Candida krusei IFC	
29	38	61.3	1 W28867	Human brain Neurog	
30	37	59.7	455	1 R62382	IT103, tranporte
31	37	59.7	1717	1 W23331	Neuroblastoma Indi
32	37	59.7	1831	1 W23329	Microtubule-associa
33	36	58.1	1 W34205	Streptomyces trans	

PI	Tatashina A;
PT	WPL: 94-28718/36.
PT	Newly isolated tau-protein kinase I enzyme - with specificity for
PT	tau-protein providing means for prevention and treatment of
PT	Alzheimer's disease
PS	Example 4: Page 25: 30pp; English
CC	R61330 is a peptide which has been phosphorylated by human
CC	tau-protein kinase (R61326).
SQ	Sequence 34 AA;
RESULT	3
W34875	Query Match 93.5%; Score 58; DB 1; Length 34;
ID	Best Local Similarity 83.3%; Pred. No. 0.0047; 1; Indels 0; Gaps 0;
AC	Mismatches 10; Conservative 1; Mismatches 0;
DT	27-MAR-1998 (first entry)
DE	Human tau protein fragment.
KW	Antibody; phosphorylated tau protein; paired helical filament;
KW	detection; Alzheimer's disease; human.
OS	Homo sapiens.
PN	W09734145-A1
PD	18-SEP-1997.
PR	13-MAR-1996; JP-056090.
PA	(MITU) MITSUBISHI CHEM CORP.
PI	Imahori K, Ishiguro K, Park J, Saito K, Uchida T;
PR	Antibody prepared using a partial peptide containing part of
PT	phosphorylated tau protein - used for detecting Alzheimer's disease
PS	Example; Pages 36-37; 48pp; Japanese.
CC	An antibody, prepared using a partial peptide containing the
CC	phosphorylated residue of the phosphorylated tau protein, e.g. the
CC	present sequence, in a paired helical filament, can be used to
CC	detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC	protein in brain extracts or tissue fragments.
SQ	Sequence 34 AA;
RESULT	4
R39837	Query Match 93.5%; Score 58; DB 1; Length 34;
Best Local Similarity 83.3%; Pred. No. 0.0047; 1; Mismatches 1; Indels 0; Gaps 0;	
Matches 10; Conservative 1; Mismatches 0;	
QY	1 KSGYSXPSPGT 12
DB	4 RSGYSSPSPGT 15
RESULT	5
R92516	Query Match 93.5%; Score 58; DB 1; Length 67;
ID	Best Local Similarity 83.3%; Pred. No. 0.0092; 1; Mismatches 1; Indels 0; Gaps 0;
AC	Mismatches 10; Conservative 1; Mismatches 0;
DT	20-SEP-1996 (first entry)
DE	Microtubule-associated tau protein epitope correspond. to pos. 146-251.
KW	Epitope; microtubule-associated protein; tau; phosphorylation; subclass;
KW	paired helical fibre; neurofibrillary tangle; dementia; neurological;
KW	Alzheimer's disease; monoclonal antibody; brain; pathology.
OS	Synthetic.
PN	WO9604305-A1.
PD	15-FEB-1996.
PR	31-JUL-1995; EP03032.
PR	29-JUL-1994; EP-870131.
PA	(INNO-) INNOGENETICS NV.
PI	Van DE VOORDE A, Vannmechelen E;
DR	WPT; 96-129338/13.
PT	Monoclonal antibodies specific for phosphorylated tau - for improved
PT	detection and diagnosis of e.g. Alzheimer's Disease
PS	Claim 2; Page 32; 42pp; English.
CC	This is the amino acid of an epitope derived from the microtubule-
CC	associated tau protein. The phosphorylated subclass of tau protein
CC	from which this epitope originates, forms a major part of the paired
CC	helical fibres which make up neurofibrillary tangles seen in patients
CC	suffering from dementia e.g. Alzheimer's disease. The epitope is esp.
CC	isolated from patients who have recently died from Alzheimer's disease.
CC	It is used to generate monoclonal antibodies for the in vitro detection
CC	or diagnosis of brain/neurological diseases such as Alzheimer's disease
CC	or other diseases where neurofibrillary tangles are a pathological
SQ	symptom.
RESULT	6
R39837	Query Match 93.5%; Score 58; DB 1; Length 106;
Best Local Similarity 83.3%; Pred. No. 0.015; 1; Mismatches 1; Indels 0; Gaps 0;	
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 KSGYSXPSPGT 12
DB	49 RSGYSSPSPGT 60

R76937	ID	136 RSGYSSPGSPGT 147
standard; Peptide; 112 AA.	RESULT	8
AC R76937;	ID	R32708
DT 04-DEC-1995 (first entry)	AC	R32708 standard; Protein; 352 AA.
DE PHF-tau (143-554) peptide.	DT	R32708;
KW PHF-tau; paired helical filament tau protein; monoclonal antibody;	DE	15-JUN-1993 (first entry)
MAB; phosphorylation; neurological disease; Alzheimer disease;	KW	Human tau-protein.
-KW Homo sapiens.	OS	Alzheimer's disease; diagnosis; subtyping; monitoring; assay.
PN WO9517429-A.	OS	Homo sapiens.
PD 29-JUN-1995.	OS	W09517429-A.
PP 14-DEC-1994; E04146.	PN	W0930339-A.
PR 21-DEC-1993; E0-403133.	PD	18-FEB-1993.
PA (INNO-) INNOCENTIICS NV.	PP	03-AUG-1992; U06382.
PI VAN DE VOORDE A, VANDERMEEREN M, VANNECHELEN E;	PR	01-AUG-1991; US-738778.
DR WPI; 95-2406167.	PA	(VOORDE) VOORHEIS P H.
PT Novel monoclonal antibodies specific for abnormally phosphorylated	PI	Voorheis PH;
PT paired helical filament tau protein (PHF-Tau) - useful for post	DR	WPI; 93-076670/09.
PT mortem or in vitro detection of neurological diseases eg. Alzheimer's	DR	N-PSDB; Q37305.
PT disease	PT	Method for diagnosing, subtyping and monitoring Alzheimer's
PS disease - by assaying a sample of body fluid for the presence of a	PT	tau-peptide using an anti-tau antibody
CC Novel Mabs AT210 and AT210 (ICACC 92122204, 93070774) form	PS	biosource; Fig 1; 43pp; English.
CC immunological complexes with a phosphorylated epitope, given in	CC	The sequence is that one form of human tau protein (from Goedert
CC R76937, of abnormally phosphorylated tau protein (PHF-tau). The	CC	et al., PNAS USA 85: 4051-4055) which was used for the Prod.
CC Mabs are used to specifically detect PHF-tau in cerebrospinal fluid.	CC	of anti-tau peptide antibodies. These are used as part of a method
CC Sequence 112 AA;	CC	for diagnosing, subtyping or monitoring Alzheimer's disease by
QY 1 KSGYSSPGSPGT 12	CC	assaying a sample of body fluid for the presence of a tau-peptide
Db 52 RSGYSSPGSPGT 63	CC	using an anti-tau antibody or the presence of an anti-tau-peptide
RESULT 7	CC	autoantibody. The methods can be used for confirming a clinical
P91294	CC	diagnosis of Alzheimer's disease and in following the course of the
ID F91294 standard; protein; 352 AA.	CC	disease and treatment.
AC P91294	QY 1 KSGYSSPGSPGT 12	Sequence 352 AA;
DT 10-MAR-1993 (revised)	Db 136 RSGYSSPGSPGT 147	
DE Paired helical filament (PHF) core protein.		
KW Paired helical filament (PHF) core protein; Alzheimer's disease;		
OS Homo sapiens.		
PN WO930339-A.		
PD 05-MAY-1989.		
PP 19-OCT-1988; G00867.		
PR 19-OCT-1987; GB-024412.		
PA (MED) Medical Research Council.		
PI WISCHIK CM, MILSTEIN C, KLUG A;		
DR WPI; 89-15054/20		
PT Paired helical filament core protein - used for providing reagents		
*PT sensitive to neurofibrillary tangles used for diagnosing Alzheimer's		
PS disease.		
DISCLOSURE: fig 1; 29pp; English.		
Paired helical filament core protein was sequenced from DNA obtained		
from brain tissue control. Alzheimer neurofibrillary tangles, The protein		
can be used to make Mab's to the PHF core or nucleotide probes, used to		
diagnose Alzheimer's disease. The protein sequence QTVYKTP (AAs 218-223)		
See also N91707.		
Sequence 352 AA;		
QY 1 KSGYSSPGSPGT 12		
CC		
Query Match 93.5%; Score 58; DB 1; Length 352;		
Best Local Similarity 83.3%; Pred. No. 0.048; 1; Mismatches 1; Indels 0; Gaps 0;		
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		

CC	Pick's disease or progressive supranuclear palsy. This sequence of the human tau protein is truncated at amino acid residue 390. The full length protein is given in W05282.	PT	cpd's, partic. phenothiazine cpds., for treating pathological
CC	Sequence 390 AA;	PT	tau-tau or neurofilament aggregation.
CC		PS	Example 2; page 53-54; 97pp; English.
DE	Detecting an agent which modulates or inhibits tau-protein association comprises contacting two tau proteins, distinct from each other yet capable of binding to the other and where one of the tau proteins is labelled, in the presence of the agent suspected of being capable of modulating or inhibiting tau-tau interaction.	CC	Agents identified as being modulators or inhibitors of tau-tau interaction may be used for the prophylaxis and treatment of
KW	Alzheimer's disease, motor neurone disease, Lewy body disease, Pick's disease or progressive supranuclear palsy.	CC	Alzheimer's disease, motor neurone disease, Lewy body disease, Pick's disease or progressive supranuclear palsy.
OS	Sequence 441 AA;	SQ	
RESULT	10		
ID	R58010 standard; protein; 441 AA.		
ID	R58010;		
DT	27-MAR-1995 (first entry)		
DE	Human tau protein.		
KW	tau; cerebrospinal fluid; immunoassay; antibody; detection; diagnosis; central nervous system; CNS; cytopathies; cytopathy; Alzheimer's disease.		
OS	Homo sapiens.		
PN	WO918550-A.		
PD	18-AUG-1994.		
PF	10-FEB-1994; JPO196.		
PR	12-FEB-1993; JP-046133.		
PA	(TEIJIN) TEIJIN LTD.		
PI	Eguchi H, Hosoda K, Kobayashi S, Kubota T, Mori H;		
PI	Nakamoto T,		
DR	WPI; 94-27910/34.		
PT	Sandwich immunoassay of tau protein in cerebrospinal fluid - for diagnosis of Alzheimer's disease and other CNS cytopathies		
PS	Claim 1; Page 15-18; 36pp; Japanese.		
CC	Detection of the human tau protein (or fragments of it) in samples of cerebrospinal fluid enables the diagnosis of central nervous system cytopathies such as Alzheimer's disease. Detection is performed using labelled antibodies which recognise sites within the region defined by the amino acid residues 251-441. The antibodies are preferably polyclonal.		
CC	Sequence 441 AA;		
SQ			
Query Match	93.5%; Score 58; DB 1; Length 441;	Query Match	93.5%; Score 58; DB 1; Length 441;
Best Local Similarity	83.3%; Pred. No. 0.06;	Best Local Similarity	83.3%; Pred. No. 0.06;
Matches	10; Conservative	Matches	10; Conservative
QY	1 KSGYSXPSPGT 12	QY	1 KSGYSXPSPGT 12
Db	194 RSGYSSPGSPGT 205	Db	194 RSGYSSPGSPGT 205
RESULT	11	RESULT	12
ID	W05282 standard; Protein; 441 AA.	ID	W34856 standard; protein; 441 AA.
AC	W05282;	AC	W34856;
DT	20-DEC-1996 (first entry)	DT	27-MAR-1998 (first entry)
DE		DE	Human tau protein.
KW	Human-tau protein; paired helical filament; detection; Alzheimer's disease; human.	KW	Antibody; phosphorylated tau protein; paired helical filament; Homo sapiens.
OS		OS	
PN	W09734145-AI.	PN	W09734145-AI.
PD	18-SEP-1997.	PD	13-MAR-1997; JPO804.
PR	13-MAR-1997; JP-056090.	PR	13-MAR-1996; JP-056090.
PA	(MITU) MITSUBISHI CHEM CORP.	PA	
PI	Inahori K, Ishiguro K, Park J, Sato K, Uchida T;	PI	
DR	WPI; 97-470918/43.	DR	
PT	Antibody prepared using a partial peptide containing part of phosphorylated tau protein - used for detecting Alzheimer's disease	PT	
PS	Claim 2; Pages 25-27; 48pp; Japanese.	PS	
CC	An antibody, prepared using a partial peptide containing the phosphorylated residue of the phosphorylated tau protein, e.g. the present sequence, in a paired helical filament, can be used to detect Alzheimer's disease, i.e. by detecting phosphorylated tau	CC	
CC	protein in brain extracts or tissue fragments.	CC	
SQ	Sequence 441 AA;	SQ	
Query Match	93.5%; Score 38; DB 1; Length 441;	Query Match	93.5%; Score 38; DB 1; Length 441;
Best Local Similarity	83.3%; Pred. No. 0.06;	Best Local Similarity	83.3%; Pred. No. 0.06;
Matches	10; Conservative	Matches	10; Conservative
QY	1 KSGYSXPSPGT 12	QY	1 KSGYSXPSPGT 12
Db	194 RSGYSSPGSPGT 205	Db	194 RSGYSSPGSPGT 205
RESULT	13	RESULT	13
ID	R36557 standard; peptide; 9 AA.	ID	R36557;
AC	R36557;	AC	R36557;
DT	10-AUG-1993 (first entry)	DT	Peptide sequence for abnormally phosphorylated tau protein.
DE		DE	Alzheimer's disease; Down's syndrome; Pick's disease; monoclonal; antibody; detection; SSPE; antigen.
KW		KW	
OS		OS	
PT		PT	
DR		FT	Key location/qualifiers
WPI;		FT	modified_site 3
NSDB; T39591.		FT	misc_difference 6 /note= "may be phosphorylated"
PT	Assay for inhibitors of tau-tau interaction - used for identifying		

FT /note- "may be phosphorylated"
 PN WO9308302-A.
 PD 29-APR-1993.
 PR 17-OCT-1992; EP-402871.

PA (INNO-) INNOGENETICS NV SA.
 PI Mandelkow E; Mercken M; Van DE VOORDE A; Vandermeiren M;
 DR WPI; 93-152493/18.

PT Monoclonal antibodies binding abnormal micro-tubule-associated
 PT tau-protein - for diagnosing neurological disorders e.g.
 PT Alzheimer's disease, Down's syndrome, Pick's disease, etc.

PS Claim 8; Page 36; 47PP; English.

The peptide is able to form an immunogenic complex with a
 monoclonal antibody contg. a phosphorylated epitope of an antigen
 belonging to human abnormally phosphorylated tau protein which can be
 obt'd from a brain homogenate isolated from the cerebral cortex of a
 patient having Alzheimer's disease. The monoclonal antibody is able
 to specifically detect only abnormally phosphorylated tau protein and
 not react with normal tau protein, and thus may be used in the detection
 or diagnosis of neurological diseases, e.g. Alzheimer's disease, Down's
 syndrome, Pick's disease or SSPE.

CC See also R36556.

CC Sequence 9 AA;

Query Match 74.2%; Score 46; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.5e-05; ID R37554
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC

QY 4 YSXPGSPGT 12
 DB 1 YSSPGSPGT 9

RESULT 15
 ID R37554 standard; peptide; 12 AA.
 AC R37554
 DT 01-OCT-1993 (first entry)
 DE Phosphorylated tau protein epitope.
 DR Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
 KW treatment; formation; Inhibition; inhibitor.
 OS Homo sapiens.
 PN EP-54442-A.
 PD 09-JUN-1993.
 PF 05-DEC-1991; 120374.
 PR 06-DEC-1991; EP-120974.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Biernat J; Drewes G; Lichtenberg-Kraag B; Mandelkow EM; Steiner B;

PS WPI; 93-18341/23

PT phosphorylated tau protein epitope associated with Alzheimer's
 disease - is used as protein kinase inhibitor for treatment and
 diagnosis.
 PS Claim 4; Page 16; 34PP; English.

CC The sequence is that of an epitope of tau protein which specifically
 occurs in a phosphorylated state in tau protein from Alzheimer's

CC paired helical fragments. It may be used as part of a method for the
 CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may
 also be used in an in vitro model for the study of the generation of
 CC the Alzheimer state of proteins and the testing of substances which
 CC prevent the conversion of normal to Alzheimer tau protein. The
 CC epitope occurs at residues 197-208 of human tau protein.

SQ Sequence 12 AA:

Query Match 74.2%; Score 46; DB 1; Length 12;
 Best Local Similarity 88.9%; Pred. No. 0.13; ID R37554
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC

QY 4 YSXPGSPGT 12
 DB 1 YSSPGSPGT 9

Search completed: October 2, 2000, 18:01:53
 Job time: 1781 sec

FT protein kinases present in mammalian brain which phosphorylate the
 CC different epitopes are also claimed but no sequences are given.
 CC Sequence 12 AA;

CC

Query Match 74.2%; Score 46; DB 1; Length 12;
 Best Local Similarity 88.9%; Pred. No. 0.13; ID R37554
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC

QY 4 YSXPGSPGT 12
 DB 1 YSSPGSPGT 9

RESULT 15
 ID R37554 standard; peptide; 12 AA.
 AC R37554
 DT 01-OCT-1993 (first entry)
 DE Phosphorylated tau protein epitope.
 DR Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
 KW treatment; formation; Inhibition; inhibitor.
 OS Homo sapiens.
 PN EP-54442-A.
 PD 09-JUN-1993.
 PF 05-DEC-1991; 120374.
 PR 06-DEC-1991; EP-120974.

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CC paired helical fragments. It may be used as part of a method for the

CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may

also be used in an in vitro model for the study of the generation of

CC the Alzheimer state of proteins and the testing of substances which

CC prevent the conversion of normal to Alzheimer tau protein. The

CC epitope occurs at residues 197-208 of human tau protein.

SQ Sequence 12 AA:

Query Match 74.2%; Score 46; DB 1; Length 12;
 Best Local Similarity 88.9%; Pred. No. 0.13; ID R37554
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC

QY 4 YSXPGSPGT 12
 DB 1 YSSPGSPGT 9

RESULT 15
 ID R37554 standard; peptide; 12 AA.
 AC R37554
 DT 01-OCT-1993 (first entry)
 DE Phosphorylated tau protein epitope.
 DR Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
 KW treatment; formation; Inhibition; inhibitor.
 OS Homo sapiens.
 PN EP-54442-A.
 PD 09-JUN-1993.
 PF 05-DEC-1991; 120374.
 PR 06-DEC-1991; EP-120974.

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 PS Claim 4; Page 16; 34PP; English.

CC The sequence is that of an epitope of tau protein which specifically

occurs in a phosphorylated state in tau protein from Alzheimer's

CC paired helical fragments. It may be used as part of a method for the

CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may

also be used in an in vitro model for the study of the generation of

CC the Alzheimer state of proteins and the testing of substances which

CC prevent the conversion of normal to Alzheimer tau protein. The

CC epitope occurs at residues 197-208 of human tau protein.

SQ Sequence 12 AA:

Query Match 74.2%; Score 46; DB 1; Length 12;
 Best Local Similarity 88.9%; Pred. No. 0.13; ID R37554
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC

QY 4 YSXPGSPGT 12
 DB 1 YSSPGSPGT 9

RESULT 15
 ID R37554 standard; peptide; 12 AA.
 AC R37554
 DT 01-OCT-1993 (first entry)
 DE Phosphorylated tau protein epitope.
 DR Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
 KW treatment; formation; Inhibition; inhibitor.
 OS Homo sapiens.
 PN EP-54442-A.
 PD 09-JUN-1993.
 PF 05-DEC-1991; 120374.
 PR 06-DEC-1991; EP-120974.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Biernat J; Drewes G; Lichtenberg-Kraag B; Mandelkow EM; Steiner B;

PS WPI; 93-18341/23

PT phosphorylated tau protein epitope associated with Alzheimer's

disease - is used as protein kinase inhibitor for treatment and

diagnosis.
 PS Claim 4; Page 16; 34PP; English.

CC The sequence is that of an epitope of tau protein which specifically

occurs in a phosphorylated state in tau protein from Alzheimer's

CC paired helical fragments. It may be used as part of a method for the

CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may

also be used in an in vitro model for the study of the generation of

CC the Alzheimer state of proteins and the testing of substances which

CC prevent the conversion of normal to Alzheimer tau protein. The

CC epitope occurs at residues 197-208 of human tau protein.

SQ Sequence 12 AA:

Tue Oct 3 09:21:57 2000

us-09-142-613-2.rag

On protein - protein search, using sw model

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Run on: October 2, 2000, 17:33:18 ; Search time 137.53 Seconds
 (without alignments), 5.400 Million cell updates/sec

Title: US-09-142-613-2

perfect score: 62

Sequence: 1 KSGYSXPSPGT 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 178050 seqs, 61884766 residues

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_64;*

1: pir1;**
 2: pir2;**
 3: pir3;**
 4: pir4;**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	58	93.5	316	1 ORHUT2
2	58	93.5	341	2 B2B820
3	58	93.5	364	2 A2B820
4	58	93.5	374	2 S4F254
5	58	93.5	402	1 QRSOT2
6	58	93.5	432	2 JSU306
7	58	93.5	441	1 ORHUT1
8	58	93.5	448	1 QRSOT1
9	58	93.5	486	2 A3D235
10	58	93.5	733	2 A45301
11	44	71.0	295	2 T1K220
12	44	71.0	315	2 T45928
13	43	69.4	351	2 R75621
14	43	69.4	553	2 T1K894
15	42	67.7	1986	2 S2B353
16	42	66.1	178	2 A3D752
17	41	66.1	330	2 S4G657
18	41	66.1	515	2 H75589
19	41	66.1	2	2 A2019
20	41	66.1	963	2 T1K140
21	41	66.1	1742	2 S2A600
22	41	65.1	558	2 T1K931
23	40	64.5	680	2 S3K216
24	40	64.5	756	2 A55943
25	40	64.5	1345	3 T2K090
26	40	64.5	1387	2 JC5502
27	40	64.5	1744	2 S4G991
28	40	64.5	1758	2 T2K350
29	40	64.5	1759	2 T2K351

ALIGNMENTS

RESULT 1

ORHUT2 microtubule-associated protein tau, fetal (clone p18) - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 02-Sep-1997

C;Accession: PN001

R;Lee, G.; Neve, R.L.; Kosik, K.S.

Neuron 2, 16:1624, 1989

A;Title: The microtubule binding domain of tau protein.

A;Reference number: JN0009; MUID:90180482

A;Cross-references: GDB:119434; OMM:157140

A;Molecule type: mRNA

A;Residues: 1-316 <LEE>

A;Note: this sequence differs from a previously reported fetal tau protein sequence o

A;Genes: MAP; MTBL1

A;Accession: PN001

F;158-188/Domain: MAP2/tau repeat homology <MT2>

F;189-219/Domain: MAP2/tau repeat homology <MT1>

F;220-251/Domain: MAP2/tau repeat homology <MT3>

Query Match Similarity 93.5%; Score 58; DB 1; Length 316;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KSGYSXPSPGT 12

Db 100 RSGYSSPGSPGT 111

RESULT 2

B2B820 microtubule-associated protein tau type 2 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

C;Accession: B2B820

R;Lee, G.; Cowan, N.; Kirschner, M.

Science 219, 285-288, 1988

A;Title: The primary structure and heterogeneity of tau protein from mouse brain.

A;Reference number: A94298; MUID:88099510

A;Accession: B2B820

A;Molecule type: mRNA

A;Residues: 1-341 <LEE>

A;Cross-references: GB:M18775; PIDN:AAA0165; PDB:g20115

C;Superfamily: microtubule-associated protein tau: MAP2/tau repeat homology

C;Keywords: alternative splicing; microtubule binding; tandem repeat

F;183-213/Domain: MAP2/tau repeat homology <MT1>

F;214-244/Domain: MAP2/tau repeat homology <MT2>

abscisic acid acti
 biotin carboxylase
 endoglucanase B pr
 outer membrane ush
 collagen alpha 3(I)
 hypothetical prote
 hypothetical prote
 probable expressio
 aldehyde dehydroge
 collagen alpha 1(X)
 hypothetical prote
 homocytic protein H
 hypothetical prote
 probable serine pr
 microtubule-associ
 microtubule-associ

F:245-276/Domain: MAP2/tau repeat homology <MT3>

RESULT 3

A28820 microtubule-associated protein tau type 1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

C;Accession: A28820

R;See: G.; Cowan, N.; Kirschner, M.

A;Title: The primary structure and heterogeneity of tau protein from mouse brain.

A;Reference number: A94298; MUID:88099510

A;Accession: A28820

A;Molecule type: mRNA

A;Residues: 1-364 <LEE>

A;Cross-references: GB:M18776; NID:920116; PIDN:AA40166-1; PID:920117

C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C;Keywords: alternative splicing; microtubule binding; tandem repeat

F:183-213/Domain: MAP2/tau repeat homology <MT1>

F:214-244/Domain: MAP2/tau repeat homology <MT2>

F:245-276/Domain: MAP2/tau repeat homology <MT3>

Query Match 93.5%; Score 58; DB 2; Length 341;

Best Local Similarity 83.3%; Pred. No. 0.022; 1; Mismatches 1; Indels 0; Gaps 0;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 4

S46264 microtubule-associated protein - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 13-Aug-1999

C;Accession: S46264

R;Sadot, E.; Marx, R.; Barg, J.; Benar, L.; Ginzburg, I.

J. Mol. Biol. 241, 325-331, 1994

A;Title: Complete sequence of 3'-untranslated region of tau from rat central nervous sys

A;Reference number: S46264; MUID:9434997

A;Accession: S46264

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-374 <SA>

A;Cross-references: EXPB:X79321; NID:9517393; PIDN:CA55889-1; PID:9517394

C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

F:185-215/Domain: MAP2/tau repeat homology <MT1>

F:216-246/Domain: MAP2/tau repeat homology <MT2>

F:247-277/Domain: MAP2/tau repeat homology <MT3>

F:278-309/Domain: MAP2/tau repeat homology <MT4>

Query Match 93.5%; Score 58; DB 2; Length 374;

Best Local Similarity 83.3%; Pred. No. 0.024; 1; Mismatches 1; Indels 0; Gaps 0;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 5

OY 1 KSGYSSXPSPGT 12

Db 127 RSGYSSPSPGT 138

Query Match 93.5%; Score 58; DB 2; Length 402;

Best Local Similarity 83.3%; Pred. No. 0.026; 1; Mismatches 1; Indels 0; Gaps 0;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 6

JS0306 microtubule-associated protein tau - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Dec-1993

C;Accession: JS0306; A33574

R;Kosik, K.S.; Orechko, L.D.; Bakalis, S.; Neve, R.L.

Neuron 2, 1389-1397, 1989

A;Title: Developmentally regulated expression of specific tau sequences.

A;Reference number: JS0306; MUID:90180457

A;Accession: JS0306

A;Molecule type: mRNA

A;Residues: 1-432 <RC>

A;Note: the sequence shown is from adult rat brain

A;Note: the partial sequence was found in the paired helical filaments character

R;Kanai, Y.; Takemoto, R.; Oshima, T.; Mori, H.; Ihara, Y.; Yanagisawa, M.; Masaki, T.

J. Cell Biol. 109, 1173-1184, 1989

A;Title: Expression of multiple tau isoforms and microtubule bundle formation in fibroblast
A;Reference number: A33574; MUID:89359509
A;Accession: AJ3574
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-132 <RAN>
A;Note: a variant lacking residues 63-91 was also found
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C;Keywords: alternative splicing; Alzheimer's disease; calmodulin binding; microtubule
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1992 #sequence_revision_30-Sep-1992 #text_change 22-Jun-1999
C;Accession: A31939; S04105; A48885; A28173; B3374
C;Cross-references: EMBL:EMBL:EMBL:X61374; NID:936722; PID:936723
R;Himler, A.; Drechsler, D.; Kirchner, M.W.; Martin, Jr., D.W.
Mol. Cell. Biol. 9, 1381-1388, 1989
Biochemistry 31, 10626-10633, 1992
A;Title: structure and novel exons of the human tau gene.
A;Reference number: S26662; MUID:93041757
A;Accession: S26665
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 187-274 <AN2>
A;Cross-references: EMBL:X61374; NID:936722; PID:936723
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991.
A;Accession: S26662
A;Molecule type: DNA
A;Residues: 371-441 <AN2>
A;Cross-references: EMBL:X61373
R;Jakes, R.; Novak, M.; Davison, M.; Wischik, C.M.
EMBO J. 10, 2215-2229, 1991
A;Title: Identification of 3- and 4-repeat tau isoforms within the PHF in Alzheimer's disease
A;Reference number: S11302; MUID:92007714
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 208-274,306-395 <JAK2>
R;Hasegawa, M.; Morishima-Kawashima, M.; Takio, K.; Suzuki, M.; Titani, K.; Ihara, Y.
J. Biol. Chem. 267, 17047-17054, 1992
A;Title: Protein sequence and mass spectrometric analyses of tau in the Alzheimer's disease
A;Accession: A43444; MUID:92381012
A;Molecule type: protein
A;Residues: 273,103-130,151-180,191-254,260-269,275-290,299-317,322-340,344-347,354-
N;Contains: microtubule-associated protein tau type II; microtubule-associated protein tau
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1990 #sequence_revision_03-May-1995 #text_change 22-Jun-1999
C;Accession: JS3370; A30217; JN0009; S03796; S26665; S26666; S26667; S17352; A43444; A277
R;Goedert, M.; Spillantini, M.G.; Jakes, R.; Rutherford, D.; Crowther, R.A.
Neuron 3, 519-526, 1989
A;Title: Multiple isoforms of human microtubule-associated protein tau: sequences and localization
A;Reference number: JS0370; MUID:90380393
A;Molecule type: mRNA
A;Residues: 1-441 <GOE>
A;Note: six isoforms are found: the clone htau40 sequence is shown. Residues 45-73, 74-100
the clone htau24 sequence lacks inserts 1 and 2; the clone htau37 sequence lacks insert
R;Goedert, M.; Wischik, C.M.; Crowther, R.A.; Waller, J.E.; Klug, A.
Proc. Natl. Acad. Sci. U.S.A. 85, 4051-4055, 1988
A;Title: Cloning and sequencing of the cDNA encoding a core protein of the paired helical
A;Reference number: A30217; MUID:88234557
A;Accession: A43444
A;Molecule type: mRNA
A;Residues: 1-44,103-274,306-441 <GO2>
A;Cross-references: GB:JN0378; NID:9338684; PIDN:AAA60615.1; PID:9338685
R;Lee, G.; Neve, R.L.; Kosik, K.S.
Neuron 2, 1615-1624, 1989
A;Title: The microtubule binding domain of tau protein.
A;Reference number: JN0009; MUID:90180482
A;Accession: JN0009
A;Molecule type: mRNA
A;Residues: 1-44,103-274,306-441 <LEE>
R;Goedert, M.; Spillantini, M.G.; Potier, M.C.; Ullrich, J.; Crowther, R.A.
EMBO J. 8, 393-399, 1989
A;Title: Cloning and sequencing of the cDNA encoding an isoform of microtubule-associate
A;Reference number: S03796; MUID:89251564
A;Accession: S03796
A;Molecule type: mRNA
A;Residues: 1-44,103-441 <GO3>
A;Cross-references: EMBL:EMBL:EMBL:X61374; NID:936724; PIDN:CAA32636.1; PID:936725
R;Andreadis, A.; Brown, W.M.; Kosik, K.S.
Biochemistry 31, 10626-10633, 1992
A;Title: structure and novel exons of the human tau gene.
A;Reference number: S26662; MUID:93041757
A;Accession: S26665
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
RESULT 7
QB01 Query Match 93.5%; Score 58; DB 2; Length 432;
Best Local Similarity 83.3%; Pred. No. 0.028; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSGYSXPSPGT 12
Db 185 RGYSSPGSPGT 195
Db 185 RGYSSPGSPGT 196
RESULT 8
QB01 Query Match 93.5%; Score 58; DB 1; Length 441;
Best Local Similarity 83.3%; Pred. No. 0.028; 1; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSGYSXPSPGT 12
Db 194 RGYSSPGSPGT 205
Db 194 RGYSSPGSPGT 205

A;Cross-references: GB:M26157; NID:951493; PIDN:AAA30770.1; PID:9514914
 R;Iqbal, K.; Grundke-Iqbali, I.; Smith, A.J.; George, L.; Tung, Y.C.; Zaidi, T.
 Proc. Natl. Acad. Sci. U.S.A. 86: 5646-5650, 1989
 A;Title: Identification and localization of a tau-peptide to paired helical filaments of
 A;Reference number: A33914; MUID:89315854
 A;Accession: A33914
 A;Molecule type: protein
 A;Residues: 28, A, 30-38, 'IG', 41, 'AP', 44, 'IK' <IQB>
 A;Experimental source: brain
 A;Note: 40-Pro was also found
 R;Iqbal, K.; Smith, A.J.; Zaidi, T.; Grundke-Iqbali, I.
 FEBS Lett. 248: 87-91, 1989
 A;Title: Microtubule-associated Protein tau. Identification of a novel peptide from bovin
 A;Reference number: S04005; MUID:89252057
 A;Accession: S04005
 A;Molecule type: protein
 A;Residues: 28, A, 30-38, 'IG', 41, 'AP', 44, 'IK' <IQ2>
 A;Experimental source: brain
 A;Note: 40-Pro was also found
 R;Paudel, H.K.; Lew, J.; Ali, Z.; Wang, J.H.
 J. Biol. Chem. 268: 23512-23518, 1993
 A;Title: Brain proline-directed Protein kinase phosphorylates tau on sites that are abnd
 A;Residues: X, 203-208, X, 23512-23518, 1993
 A;Experimental source: brain
 A;Note: sequence modified after extraction from NCBI backbone
 R;Aizawa, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.
 J. Biol. Chem. 263: 7703-7707, 1988
 A;Title: Microtubule-binding domain of Tau proteins.
 A;Reference number: A28173; MUID:88227970
 A;Accession: A28173
 A;Molecule type: protein
 A;Residues: 205-218, X, 220-223 <AI2>
 A;Experimental source: brain
 C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
 C;Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
 F;1-174, 193-448;Product: microtubule-associated protein tau, form 1 #status predicted <BN43>
 F;205-223;Region: microtubule binding #status experimental
 F;259-289;Domain: MAP2/tau repeat homology <MT1>
 F;290-320;Domain: MAP2/tau repeat homology <MT2>
 F;321-351;Domain: MAP2/tau repeat homology <MT3>
 F;352-383;Domain: MAP2/tau repeat homology <MT4>
 F;202, 209-242, 248, 411;Binding site: phosphate (Ser) (covalent) (by proline-directed kinase)
 F;212/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status expe
 A;Note: sequence extracted from NCBI backbone (NCBIN:102045, NCBIPI:102046)
 A;Accession: A45301; MUID:92262443
 A;Description: First observation of mRNA for a tau-protein from murine liver and kidn
 A;Reference number: S31658
 A;Status: preliminary
 A;Accession: S31658
 A;Molecule type: mRNA
 A;Residues: T, 529-651 <KEN>
 A;Note: this sequence is inconsistent with the nucleotide translation
 A;Accession: S31658
 R;Kenner, L.; Forstner, M.; Hutter, H.; Hoeffer, G.; Kurzbauer, R.; Zatloukal, K.; Kr
 submitted to the EMBL Data Library, May 1992
 A;Reference number: A45301; MUID:92262443
 A;Accession: A45301
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: T, 529-651 <KEN>
 A;Cross-references: EMBL:Z1133; NID:954263; PIDN:CAA78121.1; PID:938834
 C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
 C;Keywords: microtubule binding; tandem repeat
 F;541-574;Domain: MAP2/tau repeat homology <MT1>
 F;575-605;Domain: MAP2/tau repeat homology <MT2>
 F;605-636;Domain: MAP2/tau repeat homology <MT3>
 F;637-668;Domain: MAP2/tau repeat homology <MT4>
 Query Match 93.5%; Score 58; DB 1; Length 448;
 Best Local Similarity 83.3%; Pred. No. 0.029;
 Matches 10; Conservative 1; Indels 0; Gaps 0;
 Qy 1 KSGYSXPSPGT 12
 Db 201 RSGYSSPGSPGT 212

RESULT 9

A38235 microtubule-associated protein, 110K tau - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 13-Aug-1999

C;Accession: A38235

R;Goedert, M.; Spillantini, M.G.; Crowther, R.A.

Proc. Natl. Acad. Sci. U.S.A. 89: 1983-1987, 1992

A;Title: Cloning of a big tau microtubule-associated protein characteristic of the perip

A;Reference number: A38235; MUID:92179305

A;Accession: A38235

A;Molecule type: mRNA

A;Residues: 1-86 <POE>

A;Cross-references: GB:W84156; NID:9207157; PIDN:AAA2204.1; PID:9207158

A;Note: sequence extracted from NCBI backbone (NCBIN:87358, NCBIPI:87359)

C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
 C;Keywords: alternative splicing; microtubule binding; tandem repeat
 F;491-527;Domain: MAP2/tau repeat homology <MT1>
 F;528-558;Domain: MAP2/tau repeat homology <MT2>
 F;559-589;Domain: MAP2/tau repeat homology <MT3>
 F;590-621;Domain: MAP2/tau repeat homology <MT4>

Query Match	93.5%	Score	58	DB	2	Length	686
Best Local Similarity	83.3%	Pred. No.	0.044				
Matches	10	Conservative	1	Mismatches	1	Indels	0
Qy	1	KSGYSXPSPGT	12				
Db	439	RSGYSSPGSPGT	450				

RESULT 10

A45301 microtubule-associated protein tau - mouse

N;Alternate names: microtubule binding protein tau

C;Species: Mus musculus (house mouse)

C;Date: 11-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 13-Aug-1999

C;Accession: A45301; MUID:92262443

R;Couchie, D.; Mavilia, C.; Georgieff, I.S.; Liem, R.K.; Shelanski, M.L.; Nunez, J.
 Proc. Natl. Acad. Sci. U.S.A. 89: 4378-4381, 1992

A;Title: Primary structure of high molecular weight tau present in the peripheral ner

A;Reference number: A45301; MUID:92262443

A;Accession: A45301

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-733 <COU>

A;Note: this sequence is inconsistent with the nucleotide translation

A;Accession: S31658

A;Molecule type: mRNA

A;Residues: T, 529-651 <KEN>

A;Cross-references: EMBL:Z1133; NID:954263; PIDN:CAA78121.1; PID:938834

C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C;Keywords: microtubule binding; tandem repeat

F;541-574;Domain: MAP2/tau repeat homology <MT1>

F;575-605;Domain: MAP2/tau repeat homology <MT2>

F;605-636;Domain: MAP2/tau repeat homology <MT3>

F;637-668;Domain: MAP2/tau repeat homology <MT4>

Query Match 93.5%; Score 58; DB 2; Length 733;
 Best Local Similarity 83.3%; Pred. No. 0.047;
 Matches 10; Conservative 1; Indels 0; Gaps 0;
 Qy 1 KSGYSXPSPGT 12
 Db 486 RSGYSSPGSPGT 497

RESULT 11

T19220 hypothetical protein C12D8.8 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C;Accession: T19220

R;McMurray, A.; Reference number: Z19092

A;Accession: T19220

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-295 <WIL>

A;Cross-references: EMBL:273969; PIDN:CAA98236.1; GSPDB:GN00023; CESP:C12D8.8
 A;Experimental source: clone C12D8
 C;Genetics:
 A;Gene: CESP:C12D8.8
 A;Map position: 5
 A;Introns: 39/3
 C;Superfamily: unassigned collagens

Query Match 71.0%; Score 44; DB 2; Length 295;
 Best Local Similarity 63.6%; Pred. No. 3; 9; Mismatches 1;保守性 7; 比较保守
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 KSGYSXPSPG 11
 Db 213 KRGYGAPGAPG 223

RESULT 12

T4592B
 reductase-like protein - *Arabidopsis thaliana*
 N;Alternate names: protein F5K10.180
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 18-Feb-2000
 C;Accession: T4592B
 R;Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Newes, H.W.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, January 2000
 A;Reference number: 223017
 A;Accession: T4592B
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-315 <NON>
 A;Cross references: EMBL:AI132960
 A;Experimental source: cultivar Columbia; BAC clone F5K20
 C;Genetics:
 A;Map position: 3
 A;Introns: 40/3; 57/3; 83/2; 112/3; 204/3; 287/3
 A;Note: F5K20.130
 C;Superfamily: aldehyde reductase

Query Match 71.0%; Score 44; DB 2; Length 315;

Best Local Similarity 61.8%; Pred. No. 4; 2; Mismatches 9; 保守性 0; 比较保守
 Matches 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SGYSXPGSPGT 12
 Db 204 SGYSXPSPGT 214

RESULT 13

Tors-related protein - *Deinococcus radiodurans* (strain R1)
 C;Species: *Deinococcus radiodurans* (strain R1)
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C;Accession: A75621
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Ma, M.; Shem, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma, S.; Smith, H.O.; Venet, J.C.; Fraser, C.M.
 Science 286: 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A;Accession: A75250; NID:20036895
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-351 <WHI>
 A;Cross-references: GB:AEL01826; NID:96460827; PIDN:AAF12581.1; PID:96460877; TIGR:DRB0C
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DRB027
 A;Map position: megaplasmid
 A;Note: plasmid MP1

Query Match 71.0%; Score 44; DB 2; Length 351;
 Best Local Similarity 58.3%; Pred. No. 6; 8; Mismatches 2; 保守性 7; 比较保守
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KSGYSXPSPGT 12
 Db 92 RDGISTAGTGT 103

RESULT 14

T19894
 hypothetical protein C41G7.3 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T19894
 R;Steward, C.
 submitted to the EMBL data library, October 1999
 A;Reference number: Z19192
 A;Accession: T19894
 A;Status: Preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-553 <WIL>
 A;Cross-references: EMBL:Z81048; PIDN:CA02840.1; GSPDB:GN00019; CESP:C41G7.3
 A;Experimental source: clone C41G7
 C;Genetics:
 A;Gene: CESP:C41G7.3
 A;Map position: 1
 A;Introns: 25/1; 81/2; 106/3; 157/1; 179/3; 245/3; 368/1; 389/3; 423/3; 517/3
 A;Accession: S28353
 A;Molecule type: DNA
 A;Residues: 1-1986 <MAY>
 A;Cross-references: EMBL:X65566; NID:95508; PID:95509
 C;Genetics:
 A;Gene: WA
 A;Introns: 96/2; 193/3; 1365/3; 1588/3
 C;Superfamily: 3'-oxacycl-[acyl-carrier-protein] synthase I homology; acyl carrier pro
 F;911-1199/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AKT>
 F;1668-1718/Domain: acyl carrier protein homology <AKT>
 F;1766-1840/Domain: acyl carrier protein homology <AKT>

Query Match 69.4%; Score 43; DB 2; Length 351;
 Best Local Similarity 58.3%; Pred. No. 6; 8; Mismatches 2; 保守性 8; 比较保守
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 SGYSXPGSPGT 12
 Db 1746 SGLSXPASPGT 1756

RESULT 15

S28353
 probable polyketide synthase - *Emericella nidulans*
 C;Species: *Emericella nidulans*, *Aspergillus nidulans*
 C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 12-Feb-1999
 C;Accession: S28353
 R;Mayorga, M.E.; Timberlake, W.E.
 Mol. Gen. Genet. 235, 205-212, 1992
 A;Title: The developmentally regulated *Aspergillus nidulans* wa gene encodes a polype
 A;Reference number: S28353; NID:93101122
 A;Accession: S28353
 A;Molecule type: DNA
 A;Residues: 1-1986 <MAY>
 A;Cross-references: EMBL:X65566; NID:95508; PID:95509
 C;Genetics:
 A;Gene: WA
 A;Introns: 96/2; 193/3; 1365/3; 1588/3
 C;Superfamily: 3'-oxacycl-[acyl-carrier-protein] synthase I homology; acyl carrier pro
 F;911-1199/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AKT>
 F;1668-1718/Domain: acyl carrier protein homology <AKT>
 F;1766-1840/Domain: acyl carrier protein homology <AKT>

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